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	First Named Inventor or Application Identifier	Raymond J. Dattwyler
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Title of Invention	Groups of Borrelia Burgdorferi And Borrelia Afzelii That Cause Lyme Disease In Humans

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APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: **Assistant Commissioner for Patents Box Patent Application Washington, D.C. 20231**

1. [ ] Fee Transmittal Form *(Submit an original, and a duplicate for fee processing)*
2. [X] Specification **[Total Pages [55]]** *(preferred arrangement set forth below)*
   - Descriptive title of the invention
   - Cross References to Related Applications
   - Statement Regarding Fed sponsored R & D
   - Reference to microfiche Appendix
   - Background of the Invention
   - Summary of the Invention
   - Brief Description of the Drawings
   - Detailed Description
   - Claim(s)
   - Abstract of the Disclosure
3. [X] Drawing(s) (35 U.S.C. 113) **[Total Sheets [8]]** [ ] Formal [X] Informal
4. [ ] Oath or Declaration/POA **[Total Pages [ ]]**
   a. [ ] Newly executed (original or copy)
   b. [ ] Copy from a prior application (37 C.F.R 1.63(d)) *(for continuation/divisional with Box 17 completed)* **[NOTE Box 5 below]**
      i. [ ] DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. 1.63(d)(2) and 1.33(b).
5. [ ] Incorporation By Reference *(useable if Box 4b is checked)* The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
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7. [X] Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
   a. [X] Computer Readable Copy
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ACCOMPANYING APPLICATION PARTS

8. [ ] Assignment Papers (cover sheet & documents)
9. [ ] 37 C.F.R. 3.73(b) Statement *(when there is an assignee)* [ ] Power of Attorney
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GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII* THAT CAUSE LYME DISEASE IN HUMANS

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/140,042, filed June 18, 1999, the entire teachings of which are incorporated herein by reference in their entirety.

GOVERNMENT SUPPORT

The invention was supported, in whole or in part, by grant AIAR37256 from The National Institutes of Health, grant RO1AI33454 from the National Institute of Infectious Disease and cooperative agreement number U50/CCU210518 from the Centers for Disease Control. The Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

Lyme disease begins at the site of a tick bite, producing a primary infection with spread of the organism to secondary sites occurring early in the course of infection. Lyme disease is a progressive multi-system disorder and is the most common vector-borne disease in both North America and Europe. This disease was first described as a focus of pediatric arthritis patients in Old Lyme, CT (Steere, A.C., *et al., Arth. Rheum.*

20:17 (1977)). The association of this syndrome with the bite of the deer tick, *Ixodes scapularis*, led to the identification of the spirochete *Borrelia burgdorferi* as the causative agent (Burgdorfer, W., *et al., Science, 216*:1317-1319 (1982)). As culture isolation of the bacterium from clinical and field samples became more efficient, Baranton and colleagues described three pathogenic genospecies, *B. Burgdorferi* sensu stricto (*B. Burgdorferi* or *B.b.s.s.*), *B. afzelii*, and *B. garinii* (Baraton, G., *et al., Int. J. Syst. Bacteriol. 42*:378-383 (1992)). These are members of a species complex, *B. burgdorferi* sensu lato, which consists of at least 10 different genospecies (Piken, R.N., *et al., J. Invest. Dermatol., 110*:211-214 (1998); Postic, D., et al., *Int. J. Syst. Bacteriol. 44*:743-752 (1994); Valsangiacomo, C.T., *et al., Int. J. Syst. Bacteriol. 47:*1-10 (1997)). *B. Burgdorferi*, *B. afzelii* and *B. garinii* are thought to be pathogenic and all are found in Europe, but in North America, *B. burgdorferi* is the only pathogenic genospecies found. Each of these three genospecies is associated with distinct clinical manifestations (Van Dam, A. P. *et al., Clin. Infect. Dis. 17*:708-717 (1993)). This implies that differences in genospecies may play an important role in the wide array of clinical manifestations observed in Lyme Disease.

As an infected tick begins to feed on a mammal, the synthesis of outer surface protein C (OspC) is induced (Schwan, T.G., *et al., Proc. Natl. Acad. Sci. 2*:2909-2913 (1995)). Thus, in early infection, OspC is the major outer membrane protein expressed by the spirochete (Fung, B.P., *et al., Infect. Immun. 62*:3213-3221 (1994); Padula, S.J., *et al., J. Clin. Microbiol., 32*:1733-1738 (1994)). Even through OspC has been demonstrated to have limited surface exposure (Cox, D.L., *et al., Proc. Natl. Acad. Sci., 93*:7973-7978 (1996); Mathiesen, M. M., *et al., Infect Immun. 66*:4073-4079 (1998)), OspC is a potent immunogen. Immunization with OspC is protective against tick-transmitted *Borrelia* infection (Gilmore Jr., R.D., *Infect Immun. 64*:2234-2239 (1999)). However, because OspC is highly variable in its sequence, the protection is limited to the *Borrelia burgdorferi* strain expressing the same immunizing OspC encoded by a specific allele. Challenge with heterologous isolates, expressing other *ospC* alleles

results in infection (Probert, W.S., *et al.*, *J. Infect. D.*, *175*:400-405 (1997)). OspC is very diverse (Jauris-Heipke, S., *et al.*, *Med. Microbiol. Immunol. 182*:37-50 (1993)). Livey *et al.* found thirty-four alleles in seventy-six *B. burgdorferi sensu lato* isolates (Livey, I., *et al.*, *Mol. Microbiol. 18*:257-269 (1995)).

Currently, Lyme Disease is treated with antibiotics. However, such treatment is not always successful in clearing the infection. Treatment is often delayed due to improper diagnosis with the deleterious effect that the infection proceeds to a chronic condition, where treatment with antibiotics is often not useful. One of the factors contributing to delayed treatment is the lack of effective diagnostic tools. W

Furthermore, while antigens such as OspC are known to be protective, in some cases the existence of multiple alleles of these antigens greatly hinders the development of vaccines based on such antigens that would protect against more than one strain of *Borrelia*. Two independent trials of first generation vaccines for the prevention of Lyme disease, recently studied the efficacy and safety of a vaccine that is based on recombinant outer surface protein A (OspA) (Sigal, L.H. *et al.*, *N. Engl. J. Med 339*:216-222, 1998; Steere, A.C. *et al.*, *N. Engl. J. Med. 339*:209-215, (1998)). However, a vaccine that consists of recombinant OspA may require frequent booster immunizations. Natural infection with *B. burgdorferi* does not elicit an antibody response to OspA, as it does against OspC. What is needed is a selection of *Borrelia* antigens that can be used to either diagnose or vaccinate against all or most forms of *Borrelia* that cause systemic disease.

Differences in the frequency of *B. burgdorferi, B. garinii, and B. afzelii* in ticks and human infection has lead to the hypothesis that the different genospecies are differentially pathogenic (Picken, R.N. *et al.*, *J. Invest. Dermatol. 110*:211-214, 1998; Van Dam, A.P. *et al.*, *Clin. Infect. Dis. 17*:708-717, 1993). Nevertheless, the number of different strains within a given genospecies and the differences between the strains of a given genospecies as well as between genospecies impose obstacles in the development of immunogenic protein compounds for use as diagnostic and vaccine agents in the

detection, prevention and treatment of Lyme disease. A number of investigators have used OspC as a serodiagnostic antigen for early Lyme disease (Fung, B.P. *et al.*, *Infect. Immun. 62*:3213-3221, 1994; Gerber, M.A. *et al.*, *J. Infect. Dis. 171*:724-727, 1995; Padula, S.J. *et al.*, *J. Clin. Microbiol. 32*:1733-1738, (1994)). In these tests, the use of OspC as a diagnostic antigen gave highly specific, but not sensitive results. However, these studies included only one *B. burgdorferi* strain and therefore only one type of OspC. Routine tests for the diagnosis of Lyme disease also use a single strain protocol and therefore a single OspC allele for detection of antibody to the sprirochete. It is not clear what mixture of OspC proteins must be used to make useful diagnostic and vaccine tools, effective against more than one Lyme disease causing strains of *Borrelia*, if not against most if not all of the invasive strains within a genospecies. Preferably, such a mixture would be effective against all invasive strains of Lyme disease *causing borrelia.*

SUMMARY OF THE INVENTION

The present invention is drawn to a composition comprising OspC polypeptides from Lyme Disease causing *Borrelia.* In one embodiment, the composition of the present invention comprises an OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of A, B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. In another embodiment, the composition of the present invention comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.

The present invention is also drawn to a method of immunizing an animal against Lyme disease, comprising administering a composition comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the composition comprises a OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A,

B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. In another embodiment of the present invention, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. The composition of the present invention together with suitable excipients and/or adjuvants is administered to an animal such that the animal develops an immune response to at least one OspC polypeptide of the composition.

The present invention is also drawn to a method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample. The method comprises contacting a host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. The amount of antibodies that have bound said OspC polypeptides or fragments thereof are measured; thereby detecting an immune response to Lyme disease causing *Borrelia*.

The present invention is also drawn to a diagnostic kit comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the diagnostic kit comprises at least one OspC polypeptide or diagnostic fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment of the present invention, the diagnostic composition comprises at least one OspC polypeptide or diagnostic fragment thereof from each of *Borrelia afzelii* OspC families A and B.

In other embodiments of the present invention, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises OspC polypeptides or fragments thereof from *Borrelia burgdorferi, Borrelia afzelii, Borrelia garinii* and combinations thereof.

The present invention is also drawn to chimeric proteins for use in the methods of the present invention. In one embodiment, the present invention is drawn to a chimeric protein comprising OspC polypeptides from two or more OspC families of Lyme Disease causing *Borrelia*. In one embodiment, the families comprise *Borrelia burgdorferi* OspC families A, B, I and K. In other embodiment, the families comprise *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises chimeric OspC polypeptides or fragments thereof from *Borrelia burgdorferi*, *Borrelia afzelii, Borrelia garinii* and combinations thereof.

The chimeric proteins of the present invention comprise at least a first and a second polypeptide of OspC, such that the first polypeptide comprises OspC from about base 26 to about base 630 of a first *ospC* gene and the second polypeptide comprises about base 28 to about base 570 of a second *ospC* gene. The chimeric proteins of the present invention can be used in the immunization and detection methods of the present invention.

The present invention provides the minimum number of *Borrelia burgdorferi* and *Borrelia afzelii* families that are responsible for systemic disease in humans and is useful for vaccines and diagnostic kits. The present invention provides a combination of proteins that, when used as a vaccine, prevent Lyme disease from becoming systemic. The proteins and chimeric proteins of the present invention can be effective in preventing of Lyme disease as well as having a therapeutic effect on established infection, for example after the tick bite is noticed by the patient. The proteins and chimeric proteins of the present invention are expected to act at the level of the tick as well as the level of the host in preventing both infection and disease due to *Borrelia burgdorferi*, *Borrelia afzelii* and/or *Borrelia garinii*. The present invention allows the development of a worldwide vaccine comprising only six proteins necessary to generate a protective immune response against all pathogenic strains of *Borrelia burgdorferi* and *Borrelia afzelii*.

The present invention also provides improved diagnostic tools. Because of the present invention, it is now possible to prepare diagnostic tools comprising OspC antigens representing the four pathogenic families of *Borrelia burgdorferi* and/or the two pathogenic families of *Borrelia afzelii,* thereby detecting clinically important exposure to pathogenic bacteria while overlooking the remainder of the families which do not cause pathogenic disease.

As demonstrated herein, a significant proportion, if not all, systemic *B. burgdorferi* sensu stricto infections in humans are associated with four *ospC* groups and that a significant portion, if not all, systematic *B. afzelii* infections in humans are associated with two *ospC* groups. Vaccines against OspC are known to be protective, but have been limited by the diversity of *ospC* (Probert, W.S. *et al., J. Infect. D. 175*:400-405, (1997)). The polypeptides of the present invention provide immunogenic proteins, fragments and chimeric proteins thereof for highly protective vaccines and diagnostics. The present invention provides a vaccine that includes one or more of these four forms of OspC. The vaccines of the present invention should be an important second level of protection against disseminated infection of the *B. burgdorferi* spirochete. Furthermore, single-stranded conformational polymorphism (SSCP) analysis described herein may provide a rapid and powerful tool to monitor vaccine efficacy by detecting rare or new invasive *ospC* groups.

New diagnostic assays of the present invention, based on major *ospC* groups A, B, I, and K are useful to identify those at risk for progressive illness. Given that OspC proteins are antigenically variable, individuals infected with one strain may produce an antibody response that is not reactive with an OspC protein from a different major group. Antibody detection using antigen preparations of the present invention, incorporating a proper mix of invasive clones of *B. burgdorferi* will be much more sensitive than the present, single strain protocols. The compositions of the present invention not only elicit humoral and cell mediated immune responses, the

compositions of the present invention are also capable of detecting both humoral and cell mediated immune response when used to test a host sample.

The present invention provides both lipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the chimeric protein has a lipidation signal, such as the lipidation signal from outer surface protein B at the 5' terminus of the gene encoding the chimera. Furthermore, the present invention provides unlipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the gene encoding the chimeric protein does not comprise a lipidation signal and the chimeric protein is not lipidated. Unlipidated OspC polypeptides, fragments thereof and chimeric proteins thereof are advantageous due to simpler production methods, improved yields of protein and simpler purification. The unlipidated chimeric proteins of the present invention unexpectedly elicit an immune response against Lyme disease causing strains of *Borrelia* at least as broadly reactive as lipidated OspC proteins that are used as a positive control. Furthermore, the unlipidated OspC chimeric proteins of the present invention elicit an immune response to more than one genospecies of Lyme disease causing strains of *Borrelia*, including genospecies and strains that are not used to generate the chimeric OspC immunogen.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic diagram of the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks.

Figure 2 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the first bleed.

Figure 3 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the second bleed.

Figure 4 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu stricto (legend).

Figure 5 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu lato (legend).

Figure 6 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia afzelii* (legend).

Figure 7 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia garinii* (legend).

Figure 8 is a Table comparing the reactivity of lipidated OspC proteins C1 and C2 against sera from patients with the indicated condition with the reactivity of the unlipidated chimeric proteins of the present invention, where the number in parentheses is the total number of sera tested in that category.

DETAILED DESCRIPTION OF THE INVENTION

As described herein, initially nineteen groups of *ospC* from *B. burgdorferi* sensu stricto were found within a small tick population (Wang, I-N., *et al., Genetics, 151*:15-30 (1999)). Major *ospC* groups were defined using the observation that *ospC* alleles are either very similar, having less than 2% sequence divergence, or very different, having greater than 8% sequence divergence, with most having greater than 14% sequence divergence.

Based on sequence divergences, alleles of *ospC* can be grouped into twenty-one major groups (Table II). To assess whether strain differences as defined by a given *ospC* group are linked to invasiveness and pathogenicity, the frequency distributions of major *ospC* groups from ticks, from the primary erythema migrans (EM) skin lesion,

and from secondary sites, principally from blood and spinal fluid, were compared. As described herein, the frequency distribution of *ospC* groups from ticks is significantly different from that of primary site infection which in turn is significantly different from secondary sites. The major *ospC* groups A, B, I and K increased in frequency from ticks to the primary site and were the only groups found in secondary sites of the infection. Therefore, three categories of major *ospC* groups are defined herein. One category is common in ticks but very rarely, if ever, causes human disease, a second category that causes only local infection at the tick bite site, and a third category that causes systemic or disseminated disease. While many *ospC* groups found in ticks were also found in primary skin lesions, the frequency distributions are significantly different between ticks and primary skin lesions (Table III). All *ospC* groups were found more or less commonly in ticks. However, only four groups are commonly found in skin lesions or secondary infections (Tables III and IV). As described herein, the primary skin lesions harbored *Borrelia* having *ospC* groups other than A, B, I or K rarely or not at all. More importantly, only these four *ospC* groups were found in secondary sites. The finding that all systemic *B. burgdorferi* sensu stricto infections are associated with four *ospC* groups has importance in the diagnosis, treatment and prevention of Lyme disease.

There is evidence that *ospC* has been transferred between strains and even between genospecies (Wang I-N, *et al., Genetics, 151*:15-30 (1998)). This is not true of *Borrelia* chromosomal genes (Dykhuizen, D.E., *et al., Proc. Natl. Acad. Sci., 30*:10163-10167 (1999); Maynard Smith, J. and Smith, N.H., *Mol. Biol. Evol., 15*:590-599 (1998)). However, *ospA* and *ospC* alleles in *B. Burgdorferi* sensu stricto are almost completely linked (Wang I-N, *et al., Genetics, 151*:15-30 (1999)). This suggests that once an *ospC* allele has been transferred into a particular background, there is little or no selection for another similar recombination event. Thus, each major *ospC* group represents a clonal population descended from a single recombination.

Twenty percent of untreated erythema migrans clear spontaneously without causing any systemic complications (Steere, A.C. *et al., Arth. Rheum. 20*:7-17, (1977)).

As demonstrated herein, this is not significantly different ($p = 0.25$ for a 2 by 2 contingency test with double dichotomy) from the percent of non-invasive strains found in the skin, suggesting that the erythema migrans that clear spontaneously are caused by non-invasive clones.

There is extensive genetic and antigenic diversity of *ospC* in all three pathogenic genospecies of *B. burgdorferi* sensu lato (Livey, I. *et al.*, *Mol. Microbiol. 18*:257-269, 1995; Masuzawa, T. *et al.*, *Clin. Diagn. Lab. Immunol. 4*:60-63, 1997; Picken, R.N. *et al.*, *J. Invest. Dermatol. 110*:211-214, 1998; Theisen, M. *et al.*, *J. Clin. Microbiol. 31*:2570-2576, 1993; Wang, I-N. *et al.*, *Genetics 151*:15-30 (1999). As demonstrated herein, only four groups of *ospC* alleles are linked to both infectivity and invasiveness, and that invasiveness is confined to a small number of *ospC* clones. It is clear that the *ospA* and *ospC* alleles are tightly linked even though they are on different plasmids (Wang, I-N. *et al.*, *Genetics 151*:15-30 (1999)). If the invasiveness is caused by allelic variation at another locus, this variation is likely to be tightly linked to the *ospC* variation. Thus, *ospC* is a good marker for human pathogenicity and perhaps its determinator. These findings have important implications not only for our understanding of the pathogenesis of this disease but for its diagnosis and prevention.

Spirochetemia is a transient phenomenon, but is presumably key in seeding secondary skin sites, the heart, joints, and nervous system, where these *Borrelia* cause the secondary and tertiary clinical manifestations of Lyme disease. All four invasive groups of *Borrelia burgdorferi* were found in isolates from blood and CSF. The one joint isolate belonged to group A. However, it can be inferred that groups not found in the blood will not be found in the joints since most if not all dissemination of *Borrelia* to secondary sites is via blood.

Normally, model organisms are used as substitutes for experiments on humans. However, this substitution works only as long as the properties of the model organism and of humans are the same for the studied phenomena. The human immune system plays a critical role which is expected to be different from the immune response in

model organisms, particularly the mouse. Humans are accidental and usually dead-end hosts while the mouse is a critical host reservoir. The field of population genetics has developed sound procedures for reaching conclusions from survey data.

The chimeric polypeptides of the present invention elicit specific immune responses to OspC. The chimeric polypeptides also elicit immune response against strains of Lyme disease causing *Borrelia* of the same genospecies as that represented by the chimeric OspC as well as Lyme disease causing *Borrelia* of different genospecies than that represented by the chimeric OspC. The immune response includes humoral responses, secretory responses, cell-mediated responses and combinations thereof in an animal treated with the compositions of the present invention. The compositions of the present invention can include additional components suitable for *in vitro* and *in vivo* use. These additional components include buffers, carrier proteins, adjuvants, preservatives and combinations thereof.

The immunogenic compositions of the present invention can be used to immunize animals including humans. Immunization is understood to elicit specific immunogenic responses as described above. As described herein, an immunogenic response includes responses that result in at least some level of immunity in the treated animal, where the animal was treated with a composition comprising at least one protein or chimeric protein of the present invention. In one embodiment, the treated animal develops immunity against infection by Lyme disease causing *Borrelia*, wherein the chimeric proteins of the present invention elicit responses against *Borrelia burgdorferi*, *Borrelia afzelii* and *Borrelia garinii*.

Immunity, as described herein, is understood to mean the ability of the treated animal to resist infection, to resist systemic infection, to overcome infection such as systemic infection or to overcome infection such as systemic infection more easily or more quickly when compared to non-immunized or non-treated individuals. Immunity can also include an improved ability of the treated individual to sustain an infection with reduced or no clinical symptoms of systemic infection. The individual may be

treated with the chimeric proteins of the present invention either proactively, e.g. once a year or maybe treated after sustaining a tick bite.

For use as a vaccine, the composition of the present invention can include suitable adjuvants, well known in the art, to enhance immunogenicity, potency or half-life of the chimeric proteins in the treated animal. Adjuvants and their use are well known in the art (see for example PCT Publication WO 96/40290, the entire teachings of which are incorporated herein by reference). The composition can be prepared by known methods of preparing vaccines. For example, the OspC proteins or chimeric proteins to be used in the compositions can be isolated and/or purified by known techniques such as by size exclusion chromatography, affinity chromatography, preparative electrophoresis, selective precipation or combinations thereof. The prepared proteins or chimeric proteins can be mixed with suitable other reagents as described above, where the chimeric protein is at a suitable concentration. The dosage of protein or chimeric protein will vary from one μg to 500 μg and depends upon the age, weight and/or physical condition of the animal to be treated. The optimal dosage can be determined by routine optimization techniques, using suitable animal models.

The composition to be used as a vaccine can be administered by any suitable technique. In one embodiment, administration is by injection, e.g. subcutaneous, intramuscular, intravenous, or intra peritoneal injection. In another embodiment, the composition is administered to mucosa, e.g. by exposing nasal mucosa to nose drops containing the proteins of chimeric proteins of the present invention. In another embodiment, the immunogenic composition is administered by oral administration. In another embodiment of the present invention the chimeric proteins are administered by DNA immunization.

Like many outer surface proteins of Borrelia, OspC is produced in the *Borrelia* spirochete with 5' lipidation. The chimeric polypeptides of the present invention can be produced in both lipidated and non-lipidated form. In one embodiment, the lipidation signal encoded by the wild type *ospC* is removed from the coding sequence, such that

the gene or chimeric gene encodes a non-lipidated OspC or chimeric OspC polypeptide. In another embodiment of the present invention, the lipidation signal of the wild type *ospC* gene is replaced with the lipidation signal of the *ospB* gene. In this embodiment, a lipidated OspC or OspC chimeric protein is produced.

The polypeptides of the present invention can be recombinantly expressed in suitable microbial hosts, wherein said hosts include, but are not limited to, bacterial hosts, such as *E. coli,* fungal hosts *S. cerevisiae,* or cell culture hosts such as mammalian cell culture or insect cell culture.

While the lack of lipidation signal allows for the production of large amounts of OspC proteins and chimeric OspC proteins, the lack of lipidation signal was previously thought to render outer surface proteins of *Borrelia* less or non-immunogenic. However, as described herein, the non lipidated chimeric polypeptides of the present invention unexpectedly elicit as broad an immunogenicity as lipidated OspC protein (Figures 2 and 3) and greater immunogenicity against strains of other genospecies (Figure 5-7) compared to the positive controls, which were lipidated OspC from B31 and lipidated OspC from C12.

The proteins and chimeric proteins of the present invention are also antigenic and therefore useful to detect or diagnose the presence of Lyme disease causing *Borrelia*, especially *Borrelia* from groups capable of causing disseminated symptoms of Lyme disease. As described herein, disseminated symptoms refers to infection outside of the erythema migrans skin lesion, e.g. infection in blood, CNS or synovia. As described herein, antigenic refers to the ability of a compound to bind products of an immune response, such as antibodies, T-cell receptors or both. Such responses can be measured using standard antibody detection assays, such as ELISA or standard T-cell activation assays.

The present invention is drawn to compositions comprising OspC polypeptides from Lyme disease causing *Borrelia* and chimeric OspC polypeptides. In one embodiment of the present invention, compositions include one or more OspC

polypeptide or fragment thereof from at least two *Borrelia burgdorferi ospC* groups, referred also herein as families, selected from the group consisting of A, B, I and K, excepting the combination consisting of two OspC polypeptides from the A and I families. In another embodiment of the present invention, the compositions of the present invention include at least one OspC polypeptide or fragment thereof from each of *Borrelia burgdorferi ospC* families A, B, I and K. In another embodiment, the composition includes at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In still another embodiment, the composition includes OspC polypeptides from at least one *Borrelia burgdorferi* OspC group or family member selected from the group consisting of A, B, I and K and at least one *Borrelia afzelii* OspC family member selected from the group consisting of A and B.

As described herein, the *ospC* families of the present invention share about 98% homology at the nucleic acid level between strains of the same family and share no more than about 92% homology at the nucleic acid level between strains of different families. Determination of homology excludes any non-*ospC* sequences. Members of the same *ospC* family have similar antigenic profiles, e.g. elicit immune response against similar strains of Lyme disease causing *Borrelia*. The chimeric proteins of the present invention unexpectedly elicit immune response to Lyme disease causing *Borrelia* of different genospecies than the genospecies from which the component polypeptides were derived. In one embodiment of the present invention, *Borrelia burgdorferi ospC* family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, PKA, TXGW and strains of *Borrelia* containing *ospC* allele OC1. In another embodiment of the present invention, *Borrelia burgdorferi ospC* family B comprises strains 35B808, 61BV3, BUR, DK7, PB3, ZS7 and strains containing *ospC* alleles OC2 and OC3. In still another embodiment of the present invention, *Borrelia burgdorferi ospC* family I comprises strains 297, HB19 and strains containing *ospC* allele OC10, wherein strain 297 is characterized by *ospC* of GenBank Accession No. L42893. In still another embodiment of the present invention, *Borrelia burgdorferi ospC* family K

comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* allele OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank Accession No. U08284.

In another embodiment of the present invention, said compositions comprise an OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In one embodiment of the present invention, *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, Pko, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB. In another embodiment of the present invention *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 143M. As described above for *Borrelia burgdorferi* the compositions also include chimeric OspC polypeptides of *Borrelia afzelii* families A and B.

In one embodiment of the present invention, the OspC polypeptide OspC polypeptide is a chimeric OspC comprising at least one OspC protein variable region or portion thereof from at least one *ospC* gene. In one embodiment of the present invention, the OspC polypeptide variable region is encoded by a nucleic acid comprising the 3' two thirds of the *OspC* gene, about nucleotide 150 to about nucleotide 519 of an *ospC* gene (or about codon 50 to about codon 173). In another embodiment of the present invention, said OspC polypeptide variable region is encoded by a nucleic acid wherein the nucleic acid comprises, for example, nucleotide 244 to about nucleotide 519 (or about codon 81 to about codon 173), nucleic acid from about nucleotide 337 to about nucleotide 519 (or about codon 112 to about codon 173), nucleic acid from about nucleotide 418 to about nucleotide 519 (or about codon 139 to about codon 173), nucleic acid from about nucleotide 244 to about nucleotide 418 (or about codon 81 to about codon 139), nucleic acid from about nucleotide 337 to about nucleotide 418 (or about codon 112 to about codon 139), and nucleic acid from about nucleotide 150 to about nucleotide 243 (or about codon 50 to about codon 81) of an *ospC* gene.

In still another embodiment, the chimeric OspC polypeptides of the present invention comprises two or more polypeptides wherein a first polypeptide is from a first *ospC* gene from about nucleotide 26 (or about codon 8) to about nucleotide 630 (or about codon 210). In another embodiment, the first polypeptide is from about nucleotide 28. In another embodiment, the first polypeptide is from about nucleotide 53. In still another embodiment, the first polypeptide is from about nucleotide 55. In another embodiment, the first polypeptide is up to about nucleotide 621 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about nucleotide 582 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about nucleotide 576 of a first *ospC* gene.

The chimeric OspC of the present invention further comprises a second polypeptide, wherein the second polypeptide is derived from a second *ospC* gene from about nucleotide 28 (or about codon 9) to about nucleotide 571 (or about codon 190).

It is understood that the polypeptides than comprise the chimeric polypeptide can include extra nucleotides or fewer nucleotides from the given *ospC* gene from which the polypeptide is derived in order to simplify the construction of the gene encoding the chimeric polypeptide, e.g. to allow for the use of convenient restriction endonuclease sites or to allow the ligation of the gene fragments such that a contiguous coding region is created. Based on the guidance provided herein, one of ordinary skill in the art would readily be able to add or remove nucleotides from the termini of the gene fragments encoding the polypeptides of the chimeric OspC protein to generate chimeric proteins of the present invention with no or only routine experimentation. Furthermore, there can be an extra about 1 to about 10 amino acids on the N- and/or C-terminus of the polypeptides and chimeric proteins of the present invention and still retain the properties of the present invention.

The present invention also includes variants or altered versions of the OspC polypeptides and nucleic acids encoding said polypeptides. As used herein, a variant of a polynucleotide or polypeptide refers to a molecule that is substantially similar to

either the entire molecule, or a fragment thereof. For example, when the molecule is a polypeptide, variant refers to an amino acid sequence that is altered by one or more amino acids, wherein either a biological function, structure or antigenicity of said sequence or combination thereof is maintained in the variant. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, *e.g.*, replacement of leucine with isoleucine. Or a variant may have "nonconservative" changes, *e.g.*, replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Similarly, when the molecule is a polynucleotide, variant refers to a sequence that is altered by one or more nucleotides. The variant may have silent variations, wherein the change does not alter the amino acid encoded by the triplet comprising said variation or the variation is not silent, that is, alterations in encoded amino acids are generated.

As used herein, the term "altered version" refers to a polynucleotide sequence or a polypeptide sequence, wherein said sequence has one or more differences with a native or wildtype version of said sequence.

In another embodiment, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence which is homologous to one or more of the chimeric sequences of the present invention, or complements thereof. Such a nucleotide sequence exhibits at least about 80% homology, or sequence identity, with one of the chimeric OspC sequences, such that the encoded protein retains the antigenicity and immunogenicity of the unaltered chimeric protein. Preferably, the homologous sequences of the present invention shares at least about 90% homology or sequence identity with the corresponding unaltered chimeric *ospC*. Particularly preferred sequences have at least about 95% homology or have essentially the same sequence.

The altered nucleic acids and homologous nucleic acids of the present invention hybridize to the corresponding chimeric *ospC* under conditions of high stringency. A general description of stringency for hybridization conditions is provided by Ausubel, F.M., *et al.*, *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and

Wiley-Interscience 1987, & Supp. 49, 2000. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus, stringency conditions, sufficient to allow hybridization of oligonucleotides to the template, can be varied by routine optimization to generate high stringency conditions.

Alternatively, conditions for stringency are as described in WO 98/40404, the teachings of which are incorporated herein by reference. In particular, examples of highly stringent, stringent, reduced and least stringent conditions are provided in WO 98/40404 in the Table on page 36. Examples of stringency conditions are shown in Table I below which is from WO98/40404 to Jacobs *et al.*,: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)‡	Hybridization Temperature and Buffer†	Wash Temperature and Buffer†
A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T_B*; 1xSSC	T_B*; 1xSSC
C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T_D*; 1xSSC	T_D*; 1xSSC
E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T_F*; 1xSSC	T_F*; 1xSSC
G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T_H*; 4xSSC	T_H*; 4xSSC
I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T_J*; 4xSSC	T_J*; 4xSSC
K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T_L*; 2xSSC	T_L*; 2xSSC
M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	<50	T_N*; 6xSSC	T_N*; 6xSSC
O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	<50	T_P*; 6xSSC	T_P*; 6xSSC
Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
R	RNA:RNA	<50	T_R*; 4xSSC	T_R*; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6($\log_{10}$[Na^+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165 M).

As used herein, "isolated" refers to nucleic acid or polypeptide that has been removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system. An isolated polynucleotide can be part of a vector and/or composition, and still be isolated in that the vector or composition is not part of its natural environment. Likewise polypeptides can be part of a composition and still be isolated in that the composition is not part of its natural environment.

The chimeric proteins of the present invention comprise OspC proteins or polypeptides as described above from two or more OspC families of Lyme disease causing *Borrelia* as described in Table II. In one embodiment of the present invention, said families comprise *Borrelia burgdorferi* OspC families A, B, I and K and *Borrelia afzelii* OspC families A and B. The chimeric proteins of the present invention comprise, for example, a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about codon 18 to about codon 210 of a first *ospC* gene. In another embodiment,

the sequence is from about codon 8. In another embodiment, the sequence is to about codon 207. In another embodiment, the sequence is to about codon 194. In still another embodiment, the sequence is to about codon 192. The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide comprising an OspC variable polypeptide encoded by nucleic acid fragments as described above. In another embodiment of the present invention, the chimeric protein comprises two or more OspC variable polypeptides as described above.

The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about codon 9 to about codon 190 of a second *ospC* gene.

For the chimeric proteins of the present invention, at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, a chimeric protein, encoded by a single nucleic acid, wherein no two adjacent polypeptides in said fusion protein are found in the same configuration in a naturally occurring OspC protein.

In still another embodiment, the OspC proteins or chimeric proteins of the present invention from *Borrelia burgdorferi* and *Borrelia afzelii* are combined in a composition.

The present invention is drawn to a method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample. The method comprises contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises one or more OspC polypeptide or diagnostic fragment thereof from two *Borrelia burgdorferi* OspC families selected from the group consisting of A, B, I and K, excluding the composition consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. The antibodies that bind the OspC polypeptides of the composition are detected or measured; thereby detecting an

immune response to Lyme disease causing *Borrelia*. In another embodiment, the composition comprises at least two *Borrelia* OspC polypeptides or diagnostic fragment thereof from two *Borrelia afzelii* OspC families selected from the group consisting of A and B. In still another embodiment, the composition comprises polypeptides from OspC from *Borrelia burgdorferi* and *Borrelia afzelii*. In still another embodiment, the composition comprises one or more polypeptides from each of *Borrelia burgdorferi* families A, B, I and K and *Borrelia afzelii* families A and B. The composition can also comprise one or more of the chimeric polypeptides of the present invention.

The present invention is also drawn to kits comprising one or more OspC polypeptides or OspC chimeric polypeptides or combinations thereof together with suitable buffers and antibody detection reagents for the detection or diagnosis of Lyme disease causing strain of *Borrelia*. In another embodiment, the kits comprise nucleic acid sufficiently homologous to the OspC polypeptides or OspC chimeric polypeptides to detect nucleic acid encoding *ospC* genes from Lyme disease causing strains of *Borrelia* together with reagents to detect positive hybridization to target DNA or reagents to specifically DNA, for example.

For the purposes of a detection kit, "homologous" refers to two or more sequences that share substantial similarity but are not identical. Two DNA sequences are "substantially similar" when at least about 95% (preferably at least about 98%) of the nucleotides match over a defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, *e.g.*, Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc., New York; Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press. For purposes of the present invention, amino acid sequences having, for example, greater than 90 percent similarity are considered substantially homologous.

The vaccine compositions of the present invention elicit humoral and cell mediated immune responses in a host. Furthermore, the diagnostic compositions of the present invention are capable of detecting both humoral and cell mediated immune response from a host sample using standard immunodiagnostic techniques.

EXEMPLIFICATION

EXAMPLE 1: - TECHNIQUES

Borrelia strains

One hundred and forty *B. burgdorferi* strains were isolated from primary erythema migrans (EM) lesions, blood or cerebrospinal fluid (CSF) of patients seen at the Lyme Disease Center at Stony Brook, New York, Lyme Disease Diagnostic Center at New York Medical College, Valhalla, New York or the private practices of the two collaborating physicians on the eastern end of Long Island or were obtained from the Centers for Disease Control (CDC). All patients met the Centers for Disease Control surveillance definition for Lyme Disease (CDC, *Morb. Mortal. Wkly. Rep. 46*:20-21, (1997)). Isolates from skin, blood and CSF were obtained using standard techniques (Barbour, A.G., *Yale J. Biol. Med. 57*:521-525, 1984; Berger, B.W. *et al., J. Clin. Microbiol. 30*:359-361, 1992; Wormser, G.P. *et al., J. Clin. Microbiol. 36*:296-298, (1998)). Punch biopsies were taken from the advancing border of the erythema migrans lesion and incubated in BSK-H medium (Sigma, St. Louis, MO) at 34°C to create a culture. There was little culture bias as determined by direct analysis of biopsy tissue compared to culture isolates (Seinost, G. *et al., Arch. Derm.*, 135:1329-1333, (1999)), unlike isolation of *B. burgdorferi* from unfed ticks (Norris, D.E. *et al., J. Clin. Microbiol. 35*:2359-2364, (1997)). In addition, twenty-two *B. burgdorferi* sensu stricto *ospC* sequences were retrieved from GenBank. The tick data used was either from GenBank or from the study of Wang *et al.* (Wang, I-N. *et al., Genetics 151*:15-30 (1999)).

DNA isolation

For isolation of genomic *Borrelia* DNA, log phase cells were harvested by centrifugation at 10,000 RPM for 30 minutes at 4°C. The bacterial pellet was resuspended in Tris/saline-buffer (10 mM Tris (pH 7.5), 150 mM NaCl). The bacteria were then pelleted and resuspended in TNE (10 mM Tris (pH 7.5) 150 mM NaCl, 1 mM EDTA). Freshly prepared lysozyme (20 mg/ml in TNE), sodium dodecyl sulfate (10%) and proteinase K (20 mg/ml) were added and the mixture was incubated at 50°C for one hour, followed by RNAse treatment. DNA was extracted with phenol/chloroform, precipitated with ethanol and resuspended in TE buffer.

Polymerase chain reaction

The *ospC* gene was amplified using PCR, as described previously (Wang, I-N. *et al.*, *Genetics 151*:15-30 (1999)). The *OspC* gene was amplified using two external primers: 5'-AAA GAA TAC ATT AAG TGC GAT ATT-3' (+), SEQ ID NO: 1, beginning at base 6; and 5'-GGG CTT GTA AGC TCT TTA ACT G-3' (-), SEQ ID NO: 4, ending at base 602. The 5' half of *ospC* was amplified using SEQ ID NO: 1 and the reverse primer, 5'-CAA TCC ACT TAA TTT TTG TGT TAT TAG-3' (-) SEQ ID NO: 2; ending at base 345. The 3' half of *ospC* was amplified using the primer, 5'-TTG TTA GCA GGA GCT TAT GCA ATA TC-3' (+), SEQ ID NO: 3, beginning at base 289, and SEQ ID NO: 4 as the reverse primer. The external primers amplified a 597 bp fragment. Amplification of the 5' half produced a 340 bp fragment while amplification of the 3' half produced a 314 bp fragment. All the base numbers and amplified fragment sizes are based on *ospC* sequence of strain B31 (GenBank accession number U01894), with start codon as base 1.

Amplification was conducted in 50µl of a solution containing Perkin-Elmer Cetus 10x PCR buffer (100 mM Tris-HC1 (pH 8.3), 500 mM KCl), 2.5 mM $MgCl_2$, deoxynucleoside triphosphates at 0.2 mM per nucleotide, 2.5 U of Taq polymerase (Perkin-Elmer/Cetus) and 0.5 µM of each primer. The amplification reaction was

carried out for forty cycles in a DNA thermal-cycler (PTC-100; MJ Research, Inc., Watertown, MA) with an amplification profile of: denaturation at 95°C for 40 seconds, annealing at 54°C for 35 seconds, and extension at 72°C for 1 min, after an initial denaturation step at 96°C for 2 min. Negative controls were included in each experiment to control for contamination.

Cold SSCP-analysis.

SSCP analysis was chosen to characterize genetic variation of the isolated *ospC* gene fragments based on its exquisitely high detection rate of DNA polymorphisms and point mutations at a variety of positions in DNA fragments (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. 86*2766-2770, (1989)). Single point mutations have been detected in fragments up to 800bp long (Michaud, J. *et al.*, *Genomics. 13*:389-394, (1992)). However, there is evidence that the ability of SSCP analysis to detect mutations begins to decline significantly as PCR fragments approach 400bp in size (Hayashi, K., *PCR Methods & Applications 1*:34-38, (1991)). Therefore, in order to achieve high efficiency of detection of nucleotide polymorphism, the length of the PCR products used herein was 340bp from the 5' half and 314bp from the 3' half of *ospC*.

Amplified *ospC* gene fragments from all one hundred and forty strains were analyzed for genetic variations by the cold SSCP protocol described by Hongyo *et al.* (Hongyo, T. *et al.*, *Nucleic. Acids Res. 21*:3637-3642, (1993)). Briefly, 5 to 15 µl of the PCR product was added to a mixture containing 4 µl 5x TBE Ficoll sample Buffer (NOVEX, San Diego, CA) and 0.4 µl 1 µM methylmercury hydroxide (Alfa Aesaer, Ward Hill, MA). The amount of the PCR product used for the SSCP analysis was estimated after visualizing the PCR product on an agarose gel with ethidium bromide. The sample mixture was heated to 95°C for 4 min, then chilled on ice prior to loading the entire 20 µl into the gel sample well. The sharpest bands were observed when the sample was applied to a pre-cast 20% TBE gel (NOVEX) electrophoresis system (ThermoFlow ETC Unit, NOVEX) with 1.25x TBE running buffer. Electrophoresis of

SSCP products was conducted at a constant temperature of 8°C for 17 h at 240 volts in order to reveal discernable mobility shifts. Gels were stained with 0.5 µl/ml ethidium bromide in 1x TBE buffer for 25 min and destained in distilled water for 30 min. Stained bands were viewed using a 340nm UV staining box. Samples that showed more than two SSCP bands were reamplified to determine whether the bands found were real alleles or the product of PCR artifacts. Side-by-side SSCP analysis was performed in order to detect even slight shifts in electrophoretic mobility.

DNA sequencing

The *ospC* gene or representatives of each mobility class were reamplified. Double-stranded PCR fragments were purified by agarose gel electrophoresis and subjected to automated DNA sequencing using fluorescent dideoxy terminator chemistry and the forward and reverse primers originally used for PCR amplification.

Statistical analysis

Chi square analysis of contingency tables was performed. This analysis tests for significant difference in frequency distributions. The tables were 2xN where N is the number of major *ospC* groups distinguished. The average expected number in each element of the table needs to be about six or greater for an unbiased test (Zar, J.H., *Biostatistical Analysis, 3rd ed*, p. 206, (1996)). This means that the number of observations should be greater than 6 times 2N. When the expected average number was less than six, the major *ospC* groups with the lowest number in the sample were combined until the number of observations were about equal to or greater than 12N.

RESULTS

ospC mobility classes in human *B. burgdorferi* isolates.

One hundred and thirty-two isolates of *B. burgdorferi* sensu stricto from patient samples of skin, blood, and CSF (Table II) were propagated *in vitro* and used as a source

of DNA for analysis. The *ospC* genotype of each strain was determined by cold SSCP analysis of the 5' end (340bp) of the gene and was confirmed by SSCP analysis of the 3' end (314bp) of *ospC*. In all *B. burgdorferi* isolates, the genetic variation at the 5' end of the gene corresponded to the variation at the 3' end. At least two representatives of each SSCP mobility class were subsequently sequenced. The sequences of the same mobility classes were identical in all samples and each mobility class had a unique sequence. Therefore, the sensitivity and specificity of SSCP analysis was 100%. Each SSCP mobility class was designated as an allele. Wang *et al.* recently described 13 *ospC* alleles (Wang, I-N. *et al.*, *Genetics 151*:15-30). An additional five *ospC* (OC) mobility classes, OC14-18 are described herein. OC14 has the same *ospC* sequence as the *ospC* in strain 2591.

TABLE II. Alignment of major *ospC* groups with *ospC* alleles identified by SSCP analysis

Major *ospC* Group	*ospC* allele (SSCP)	GenBank number[1]	Ticks	Skin[2]	Dis-seminated[2]
A	1	AF029860	17	23	21
B	2	AF029861	17	19	4
C	3	AF029862	11	3	0
D	4	AF029863	10	1	0
E	5, 7	AF029864	6	1	0
F	6	AF029865	9	0	0
G	8	AF029867	5	7	0
H	9	AF029868	7	6	0
I	10	AF029869	1	9	3
J	11, 18	AF029870	3	7	0
K	12, 13	AF029871	6	32	16
L	-	L42899	2	0	0
M	14	U01892	1	3	0
N	15	L42899	1	3	0
O	-	X84778	0	1	0
P	-	U91796	1	0	0
Q	-	U91790	1	0	0
R	-	U91791	2	0	0
S	-	U91793	1	0	0
T	16	AF065143	0	1	0
U	17	AF065144	0	2	0

[1] A single GenBank sequence of each type is given as an example.

[2] The number of each major *ospC* group observed in blood, synovial fluid or cerebrospinal fluid. This includes both SSCP data and data from the literature, including GenBank.

**B. burgdorferi* sensu stricto Groups P through S are only found in Europe. Groups R and S are excluded from the analysis because nearly identical *ospC* alleles are found in *B. afzelii* and *B. garinii*, showing these groups were recently created by cross-species transfer.

Multiple infections

Of the one hundred and thirty-two primary isolates from patients with Lyme disease in this study, most contained only a single strain. Seven skin isolates and one CSF isolate contained two different strains as determined by SSCP analysis, thus giving a total of one hundred and forty different strains. The *ospC* allele pairs found in multiply infected erythema migrans biopsy specimens were (OC1, OC12), (OC1, OC14), 2x(OC2, OC3), 2x(OC2, OC12), and (OC8, OC18). CSF isolate NY940657 contained *ospC* alleles OC1 and OC12. For CSF isolate 297, which was isolated in Connecticut, there were two *ospC* sequences published in GenBank: L42893, which is analogous to OC10 and U08284, which is analogous to OC12. The pair-wise difference of *ospC* sequences of both strains is 16.4%, suggesting CNS infection with two different strains in this isolate. Overall, 5.5% of all isolates described herein contained two strains. Because as many as 50% of ticks isolated in the wild are infected with multiple strains, exposure to multiple strains in a single tick bite is common, raising the possibility that different strains are differentially pathogenic.

To these one hundred forty strains for which the *ospC* allele was determined herein, twenty-two strains of known *ospC* sequence from GenBank were added to give a total of one hundred sixty-two. Fifty-one of these strains were obtained either from

eastern Long Island; seventy-seven were obtained from Westchester County, New York, and the remainder from other endemic areas in the United States (twenty-two strains) and Europe (twelve strains). The isolates were divided into those from the site of the primary infection, the erythema migrans skin lesion (one hundred eighteen isolates), and those from secondary sites, where the infection had disseminated (forty-four isolates). This later group included, for example, twenty from cerebro-spinal fluid (CSF), twenty-three from blood, and one from synovial fluid.

Major *ospC* groups in human *B. burgdorferi* isolates

Surprisingly, as described herein, the differences between *ospC* sequences among and between the families of *B. burgdorferi* sensu stricto fell into two groups. Pairs of *ospC* genes within the same family differed in nucleic acid sequence by less than two percent while pairs of *ospC* genes from separate families in nucleic acid sequence differed by more than eight percent. Wang *et al.*, defined nineteen major *ospC* groups, designated A to S (Wang, I-N. *et al.*, *Genetics 151*:15-30 (1999)). As described herein, two additional *ospC* groups are provided, designated T and U. OC16 represents major group T and OC17 represents major group U (Table I). The lowest pair-wise differences of group T and U to any other major *ospC* group are 16.1% and 20.5% respectively.

B. burgdorferi clones are differentially pathogenic

As described herein, clones representing different *ospC* groups of *Borrelia burgdorferi* are differentially pathogenic. This is demonstrated by the differing frequencies of the various major *ospC* groups in ticks, in the initial infection in the skin, and in disseminated infections.

The strains in GenBank and the literature for which the *ospC* sequences have been determined were widely sampled from the entire geographic range of the species and were chosen irrespective of whether they were from ticks or humans. These strains

gave a small but random sample of the frequencies of the major *ospC* groups in ticks and humans. As demonstrated herein, the frequency of the major *ospC* groups from human isolates was found to be significantly different from the frequency found in ticks on Long Island. Table III shows that the frequency distribution of strains from skin from eastern Long Island differ significantly from tick strains collected in the same area.

TABLE III

Major *ospC* groups	A	B	C	D	F	G	H	I	K	Comb.[a]
Isolates From Erythema migrans lesions (N=46)	13	6	2	0	0	1	0	4	16	4
Ixodes scapularis ticks (N=74)	12	12	11	9	6	5	7	1	5	6

$\chi^2 = 36.3$ with 9 degrees of freedom

$p<0.001$

[a] Combined major groups are defined by individual frequencies of 0.025 or less and include groups E, J, N, O.

The analysis provided herein of all *ospC* groups presented in this study showed that most groups are found in both ticks and in humans (Table II). However, major groups A, B, I and K predominated in humans, with A and K groups found most frequently. (Figure 1).

The pattern of pathogenicity of the various clones as demonstrated by frequency in the primary site of infection, the skin, compared to the frequency in secondary sites revealed that only four major groups (A, B, I and K) were found in both the skin and secondary sites (compare Tables III an IV). All other major groups were found only in the skin. When all groups with three or fewer isolates are combined to give the

combined group of Table IV, a 2 by 8 contingency test comparing the frequency distribution of skin versus secondary sites gives a significance of $p<0.005$. When no groups are combined, a 2 by 15 contingency test is still significant ($\chi^2 = 24.07$ with 14 degrees of freedom, $p<0.05$). The distribution of strains from primary and secondary sites indicated that only a certain of the major groups, A, B, I, and K cause disseminated disease. As described herein, these are referred to as invasive clones whereas other clones are referred to as non-invasive clones.

TABLE IV

Major *ospC* groups	A	B	G	H	I	J	K	Comb.[a]
Isolates From								
Erythema migrans lesions (N=118)	23	19	7	6	9	7	32	16
Disseminated Infections (N=44)	21	4	0	0	3	0	16	0

$\chi^2 = 23.6$ with 7 degrees of freedom

$p<0.005$

[a] Combined major groups are defined by individual frequencies of 0.025 or less and include groups C, D, E, M, N, O, T and U.

As described herein, the different clones of *B. burgdorferi* sensu stricto, as defined by *ospC* groups, are differentially pathogenic. Some groups very rarely, if ever, cause human disease, e.g. *ospC* groups D, E, F, and L. Some groups cause a local infection at the tick bite site, but not systemic disease, e.g. *ospC* groups G, H, J, and T. Finally, there are some groups which are responsible for systemic disease; these are

ospC groups A, B, I, and K. Our findings indicate that all systemic *B. burgdorferi* sensu stricto infections in humans are caused by strains in these four *ospC* groups.

Figure 1 shows the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks, n=72, (A); erythema migrans lesions, n=118, (B); and secondary sites of infection, n=44, (C). The percentage of group A plus K increased from 23% in the tick isolates, to 47% in the skin isolates, and to 84% in the secondary sites. The length of the bars in Figure 1 reflect this increase, by holding the length of the combined A and K groups constant. In the skin, groups C, D, E, M, N, O, T and U have been combined since their individual frequencies are 0.025 or less. This combination of groups when combined make up 12.7% of the total number of strains.

A similar analysis was conducted for *Borrelia afzelii*. The analysis included *OspC* alleles from 21 strains from GenBank and 12 strains sequenced for this study. These sequences fell into 20 major groups where the definition of a group is less that 1% sequence diversity within a group and at least 7.7% sequence difference between groups. There were two exceptions to this rule which were caused by a deletion in one *ospC* gene and a cross-species transfer of a small section of DNA in another *ospC* gene. When these anomalous sections were removed, all *ospC* alleles fell into 20 groups. Only two groups contained strains from chronic infections - groups A and B. By analogy and the *B. burgdorferi* study, it appears that only two groups are pathogenic in *B. afzelii*.

EXAMPLE 2: Protein Expression and Immunoblot

Protein Expression

The *Escherichia coli* (strain BL21 (pLysS) or strain B834 (DE3)) were transformed with the plasmid encoding the recombinant chimeric *Borrelia* proteins (RCBPs), and grown in 10 ml LB media (5 g/l NaCl, 10 g/l tryptone, 5 g/l yeast extract, 25 mg/l chloramphenicol and 50 mg/l ampicillin) at 37°C, with shaking. When the

optical density at 600λ reached 0.3-0.4 units, recombinant protein expression was induced by adding IPTG (isopropyl B-D-thiogalactopyranoside) to a final concentration of 0.5 mM and the cells were grown for an additional three hours. The cultures were harvested by centrifugation at 3800xg for five minutes. The cells were resuspended in 20 mM $NaPO_4$, pH7.7 and stored at -20°C overnight. Once thawed, the crude extracts were incubated with DNase (2 μg/ml) in the presence of 2.5 mM of $MgCl_2$ at room temperature for thirty minutes, spun at 14000 rpm (Eppendorf 5417C) for five minutes and 5 μl of the protein sample was run on a SDS-PAGE which was either stained in Commassie Blue or used for Immunoblot. Protein samples were solubilized, usually with a sodium dodecyl sulphate (SDS) containing buffer and in selected cases with reducing agents such as dithiothreitol (DTT) or 2-mercaptoethanol (2-ME). Following solubilization, the material was separated by SDS-PAGE. The proteins were then eletrophoretically transferred to a polyvinylidene difluoride membrane (PVDF, Immobilon-P®, Millipore). The transfer of proteins was monitored by a reversible staining procedure, Ponceau S. The stained membrane was made and the membrane destained by soaking in water for 10 minutes. All non-specific binding sites in the proteins and on the membrane were blocked by immersing the membrane in a solution containing a protein or detergent blocking agent (5 % milk in tris-buffered saline (TBS) Tween-20® 0.1%). The membranes were then incubated with primary antibody (either a monoclonal antibody or Erythema Migrans Lyme disease human serum). The membrane was washed and the antibody-antigen complexes were identified using alkaline phosphatase (AP) enzymes coupled to secondary antibody, either anti-immunoglobulin G (anti-mouse IgG) to detect the monoclonal antibody or anti-human IgA+IgG+IgM to detect the serum antibodies. A chromogenic substrate for alkaline phosphatase was then used to visualize the activity.

EXAMPLE 3: SEROLOGIC CHARACTERIZATION - ELISA (Enzyme-Linked Immunosorbent Assay)

Immobilization of RCBPs onto ELISA Plates, Determining Optimal RCBP Binding:

A solution of purified RCBPs in sodium phosphate buffer, pH 9.0 was used to coat commercial microwell plates (MaxiSorp®, Nunc). Recombinant OspC *Borrelia* proteins are described in Table V. The coating procedure was as follows: 100 µl of a solution containing the appropriate concentration of each RCBP was added to each well and the microwell plate was incubated for either one hour at room temperature or at 4°C overnight. The antigen solution was removed from the wells, the plate washed three times with phosphate buffered saline (PBS) pH 9.0, and 200 µl of blocking solution added (2% BSA fraction V (Sigma) in PBS). Following a thirty minute incubation at 37°C, the plates were washed three times with PBS, wrapped in plastic and stored at 4°C until used. The binding of the individual RCBPs was measured using monoclonal antibodies specific for either OspA or OspC followed (after washing) by an alkaline phosphatase-conjugated goat anti-mouse secondary antibody. The upper limit of protein binding was found to be beyond the working range of the monoclonal antibody used to measure it, and the standard blocking protocol was found to successfully saturate this high protein binding capacity, leaving low background readings in the control wells. The results of these experiments indicated that a protein concentration of 0.5 µg/ml in the coating buffer was optimal for each of the RCBP tested. It was not found to be necessary that the chimeric proteins be immobilized in a specific molar ratio to one another; only that enough of each protein be bound so that epitopes in that chimeric protein do not become limiting in subsequent ELISA assays using patient serum. For practical purposes, it was found that these conditions were met when the monoclonal-capture assay reached an absorbance of about 1.5 units or greater for each mouse monoclonal antibody, with a specific epitope represented in one of the chimeric proteins on the well surface. If necessary, however, the concentrations of individual

proteins in the mixture can be adjusted to achieve the desired levels of immobilized protein using routine optimization. Although the amount of each RCBP bound to the surface of the well and the amount of any one epitope exposed to the solution varies somewhat from protein to protein, the amount of bound epitope was not found to be limiting within the useful range of the ELISA.

ELISA Tests:

The standard procedure for the ELISA tests was as follows: human serum samples were diluted 1:100 in specimen diluent (10% fetal bovine serum in PBS pH 9.0) and 100 µl of each sample added to ELISA plate microwells that had been coated with antigen as described above. Following incubation for 1 hour at 37°C, the samples were removed and the plates washed three times in TBS-Tween™ (0.5 M Tris pH 7.2; 1.5 M NaCl; 0.5% Tween ™). Goat anti-human antisera conjugated to alkaline phosphatase specific for either IgM (Fc) or IgG (Fab), (Jackson Immuno Research Laboratories) was diluted 1:1000 in PBS, pH 7.4 and 100 µl of the solution added to each well. Following incubation for thirty minutes at 37°C, the plates were washed three times with TBS-Tween ™ and 100 µl of substrate solution (5 mg of p-nitrophenylphosphate tablets dissolved in 1X diethanolamine substrate buffer to yield a 2 mg/ml solution - Kirkegaard Perry Laboratory) was added to each well. The plates were incubated for thirty minutes at 37°C and 100 µl of stop solution (5 % EDTA) was added to each well. The absorbance at 410 nm was read on a microplate reader (Dynatech). A sample was considered positive if it produced an average absorbance greater than the mean of the negative controls plus three standard deviations. Cross-reactivity was measured against serum from patients with syphilis, systemic lupus erythematosus, rheumatoid arthritis as well as endemic field workers and non-endemic field worker.

Using the above-described ELISA test, serum from various patients was tested. Patients with Erythema Migrans Acute (EMA) had early, localized infections, typified

by the presence of well-defined erythemamigvans (EM) in patients from an endemic area. Patients with Early Disseminated (EA), are Acute Disseminated (AcD) infections were typified by EM and one of the following: additional EM lesions, AV block, neurological abnormalities (e.g., seventh nerve pasly), or meningitis. Patients with Acute Convalescent (AcC) were obtained from the same patients as EA and AcD, 2-4 weeks later. Serum was also tested from the CDC from patients with well documented Syphilis (S), serum was also obtained from SUNY at Stony Brook, Division of Rheumatology from patients with well documented systemic Lupus Erythematosus (SLE) or patients with well documented Rheumatoid Arthritis (RA). Endemic field worker sera (End), were obtained from outdoor workers from Long Island, which is endemic for Lyme disease. Non-endemic sera (Nedn) were obtained from outdoor workers from Arizona, which is not endemic for Lyme disease. In addition, serum was tested from endemic field workers (End) and non-endemic field workers (NEnd). Polypeptides of the present invention were used to test these various sera as summarized in Figure 8.

Table V

Polypeptide	SEQ ID NO.:* (DNA)	SEQ ID NO: (POLYPEPTIDE)
C1 unlipidated	5	6
C2 unlipidated	7	8
[1]C1	9	10
C2	11	12
C5	13	14
C7	15	16
C10	17	18
C11	19	20
C12	21	22
C1C10[2]	23	24
C1C12	25	26
B31C10[3]	27	28
B31C12	29	30
C2C7	31	32
C2C10	33	34
C2C12	35	36
C5C7	37	38
C5C10	39	40
C5C12	41	42

1 C1-C12 are OspC genes/proteins with lipidation signal.

2 C2C10 and other compound C names refer to chimeric OspC proteins wherein the N-terminal portion of the chimera is derived from a first *ospC* allele and the C-

terminal portion of the chimeric molecule is derived from second *ospC* allele, as described herein. The polypeptides were not lipidated.

EXAMPLE 4: MICE IMMUNIZATION WITH OSPC CHIMERIC PROTEINS AS IMMUNOGEN

Female BALB/c mice, four-five weeks old, were immunized with 5 μg of OspC chimeric proteins in 100 μl of aluminum hydroxide adjuvant by SC (subcutaneous) injection. Five mice were used for each group. For the negative control, five female BALB/c mice were immunized with 100 μl of aluminum hydroxide adjuvant only. Two weeks after immunization, the mice received a boost with the same antigen and two weeks after that an equal boost was administered. One week after each boost, blood was drawn from each mouse (including negative controls) and the serum was tested, using the ELISA method described above, for the presence of the respective anti-OspC chimeric protein antibodies.

Mice were immunized with chimeric proteins as follows in Table VI.

TABLE VI

Immunogen	SEQIDNO.:(polypeptide)	OspC Family
LipCB31[1]	44 (DNA 43)	A
LipC12[2]	22 (DNA 21)	K
UnlipC2[3]	8	B
UnlipC2C7[4]	32	B/E
UnlipC2C10	34	B/I
UnlipC2C12	36	B/K
UnlipC5C10	40	E/I
UnlipC5C12	42	E/K

1 "Lip" means lipidated N-terminus, Lip CB31 is OspC protein from *B. burgdorferi* strain B31.

2 The number immediately after "C" refers to the particular allele of OspC as described herein.

3 "Unlip" means the unlipidated form of the N-terminus.

Several types of single OspCs from *B. burgdorferi sensu stricto*, OspCB31, OspC2, OspC5, OspC7, OspC10, OspC12 and a single OspC from *B. afzelii,* Ctro, were used as the antigens in an ELISA to test the serum collected from the immunized mice. As shown in Figures 2 and 3, unlipC2C10 and unlipC2C12 elicited an immune response in the form of antibodies, (a humoral response) against a broad range of *ospC* families, after the first and second bleeds, respectively. The serum from unlipC2C10, unlipC2C12, LipCB31 and LipC12 immunized mice was then used to test against single OspC polypeptides from several strains of the three major *Borrelia* gene species *Borrelia burgdorferi, Borrelia afzelii* and *Borrelia garinii.*

As shown in Figure 4, 13 different strains of *B. burgdorferi* sensu stricto *(B.b.s.s.)* were tested for reactivity with the above described sera. Sera from mice immunized with both LipCB31 and LipC12, which were the gold standard of this

experiment, detected 12/13 of the *B.b.s.s.* strains tested. Sera from mice immunized with unlipidated C2C12 detected 8/13 of the strains tested. Use of unlipidated forms of these proteins as vaccine immunogens or diagnostic antigens is desirable because the product yield by the expression vector is much greater and the proteins are much easier to purify. These two reasons alone made the production of these proteins less expensive.

As shown in Figure 5, chimeric proteins unlipC2C10 and unlipC2C12 of the present invention elicited an immune response that detected 5/6, and 6/6 of the strains tested, as compared to the gold standard lipidated proteins LipC12 and LipCB31, which detected 5/6 and 3/6 of the strains, respectively. When compared to the parental unlipidated OspC2 (rOspC2), the chimeric proteins unlipC2C10 and unlipC2C12 elicited an immune response and detected more strains than the gold standard ((0/6) versus (5/6) and (6/6) respectively). This result was unforeseen and unexpected.

In another experiment, as shown in Figures 6 and 7, chimeric proteins of the present invention elicited a significant immune response across all the 18 different strains of *B. afzelii* (Fig. 6) and all the 21 different strains of *B. garinii* (Fig. 7). For example, the chimeras unlipC2C10 and unlipC2C12 detected 12 and 18 of the 18 strains of *B. afzelii*, respectively, as compared to 0/18 detected by the parental unlipidated C2. The same chimeras detected 14 and 20 of the 21 strains of *B. garinii*, respectively, as compared to 0/21 detected by the parental unlipidated C2. Furthermore, the gold standards LipCB31 and LipC12 detected 2 and 17 of the 18 strains of *B. afzelii*, respectively, and 2 and 15 of the 21 strains of *B. garinii*. These results indicate that, unlike the LipOspCB31, LipOspC12 and unlipOspC2, the unlipidated C2C10 and unlipidated C2C12 used as immunogens elicited a significant immune response across all the different strains of *B. burgdorferi, B. afzelii and B. garinii* tested.

Additional chimeras were constructed and are listed in Table VII.

TABLE VII

OspC Polypeptides and Chimeric Polypeptides of the Present Invention

POLYPEPTIDE	SEQ ID NO.:(DNA)	(POLYPEPTIDES)
[1]unlip OspC kkp(55-621*)	45	46
unlip OspC PKO	47	48
unlip OspC TRO	49	50
[2]unlip OspC-55B31/ 58PKO/56TRO	51	52
unlip OspC1-TRO	53	54
unlip OspC-TRO	55	56
[3]Blip OspC1C10	59	60
BlipOspC12	61	62
Blip OspC1-TR0	77	78
Blip OspC2C7	67	78
Blip OspC2C10	63	64
Blip OspC2C12	65	66
Blip OspC2-TRO	69	70
Blip OspC5C7	75	76
Blip OspC5C10	71	72
Blip OspC5C12	73	74
Blip OspCB31C10	79	80
Blip OspCB31C12	81	82
Blip OspCPkoTro	83	84
Blip OspC-55B31/58Pko/56Tro	85	86

[1]Ulip means the polypeptide is unlipidated.
[2]An OspC chimera comprised of 3 OspC polypeptides.

[3]Blip means the polypeptide is lipidated due to the gene having the OspB lipidation signal on the 5' terminus.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims.

CLAIMS

What is claimed is:

1. A composition comprising OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:

    a) said composition comprises one or more OspC polypeptides or immunogenic fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from family I, or;

    b) said composition comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia afzelii* OspC families A and B.

2. The composition of Claim 1 comprising one or more OspC polypeptides or fragments thereof from each of *Borrelia burgdorferi* families of the group of subpart a).

3. The composition of Claim 1, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.

4. The composition of Claim 3, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.

5. The composition of Claim 3, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.

6. The composition of Claim 1, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.

7. The composition of Claim 1, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.

8. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.

9. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.

10. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.

11. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC*

gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.

12. The composition of Claim 1, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.

13. The composition of Claim 1, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.

14. A method of immunizing an animal against Lyme disease, comprising administering a composition comprising at least two OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:

a) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I, or;

b) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.

15. The method of Claim 14, wherein the composition comprises one or more OspC polypeptides or fragments thereof from each of *Borrelia burgdorferi* families of the group of subpart a).

16. The method of Claim 14, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.

17. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.

18. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an ospC gene.

19. The method of Claim 14, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.

20. The method of Claim 14, wherein the *ospC* gene encoded the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.

21. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.

22. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.

23. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.

24. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.

25. The method of Claim 14, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.

26. The method of Claim 14, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.

27. A method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample, comprising;

a) contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present in said sample bind to said OspC polypeptides; wherein

i) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from family I, or;

ii) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B; and

b) detecting antibodies that have bound said OspC peptides; thereby detecting an immune response to Lyme disease causing *Borrelia*.

28. The method of Claim 27, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.

29. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.

30. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.

31. The composition of Claim 27, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.

32. The method of Claim 27, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.

33. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.

34. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.

35. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.

36. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.

37. The method of Claim 32, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.

38. The method of Claim 32, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.

39. A chimeric protein comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:

a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 26 to about nucleotide 621 of an *ospC* gene from a first OspC family and

b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

40. The chimeric protein of Claim 39, wherein said OspC families are selected from the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and *Borrelia afzelii* OspC families A and B.

41. A chimeric protein comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:

a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 53 to about nucleotide 570 of an *ospC* gene from a first OspC family and

b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

42. The chimeric protein of Claim 41, wherein said protein is unlipidated.

43. A chimeric OspC protein selected from the group consisting of: SEQ Id Nos: 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84 and 86.

44. An isolated nucleic acid encoding a chimeric protein wherein said protein comprises OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:

a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 26 to about nucleotide 621 of an *ospC* gene from a first OspC family and

b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

45. The nucleic acid of Claim 44, wherein said OspC families are selected from the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and *Borrelia afzelii* OspC families A and B.

46. The nucleid acid of Claim 44, wherein said protein is unlipidated.

47. A isolated nucleic acid comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said isolated nucleic acid comprises:

a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 53 to about nucleotide 570 of an *ospC* gene from a first OspC family and

b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

48. An isolated nucleic acid selected from the group consisting of : SEQ ID Nos: 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 51, 53, 55, 56, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83 and 85.

GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII* THAT CAUSE LYME DISEASE IN HUMANS

ABSTRACT OF THE DISCLOSURE

The present invention is drawn to an immunogenic composition comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia afzelii* OspC families A and B.

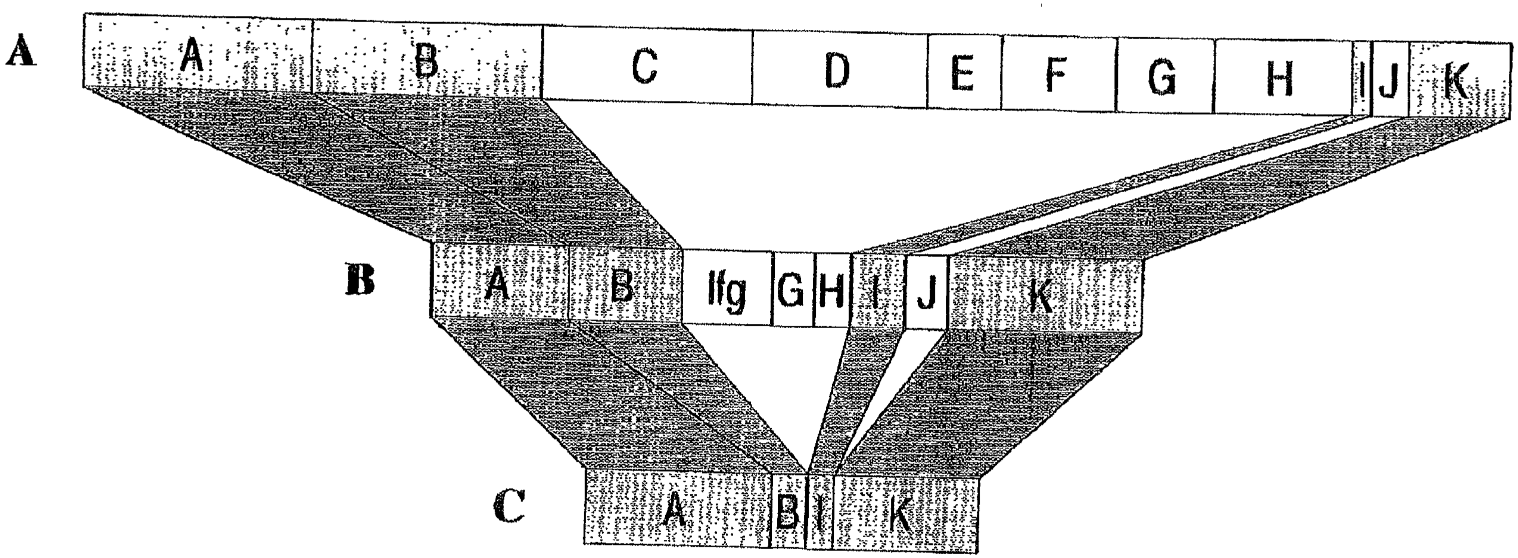


Fig. 1

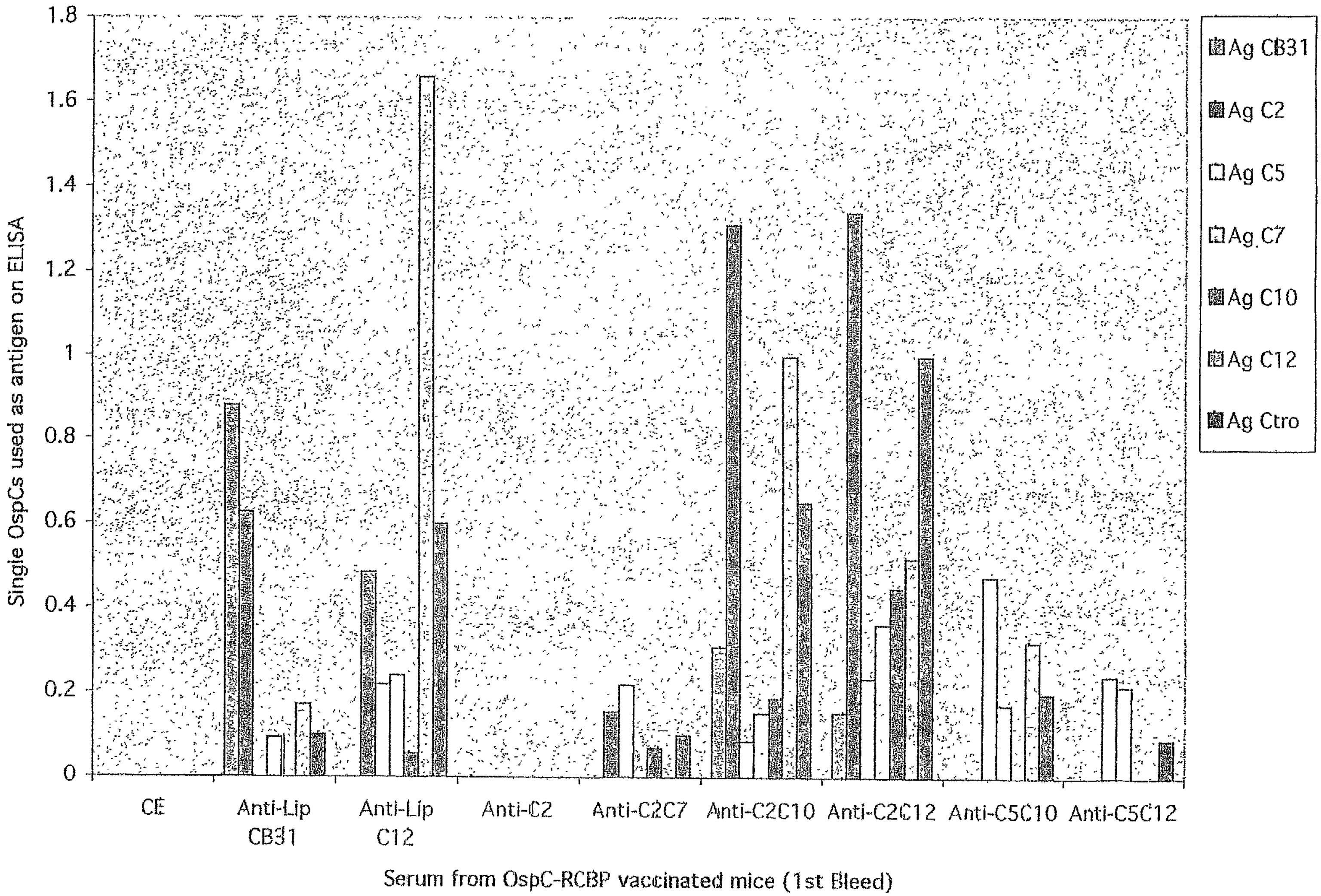
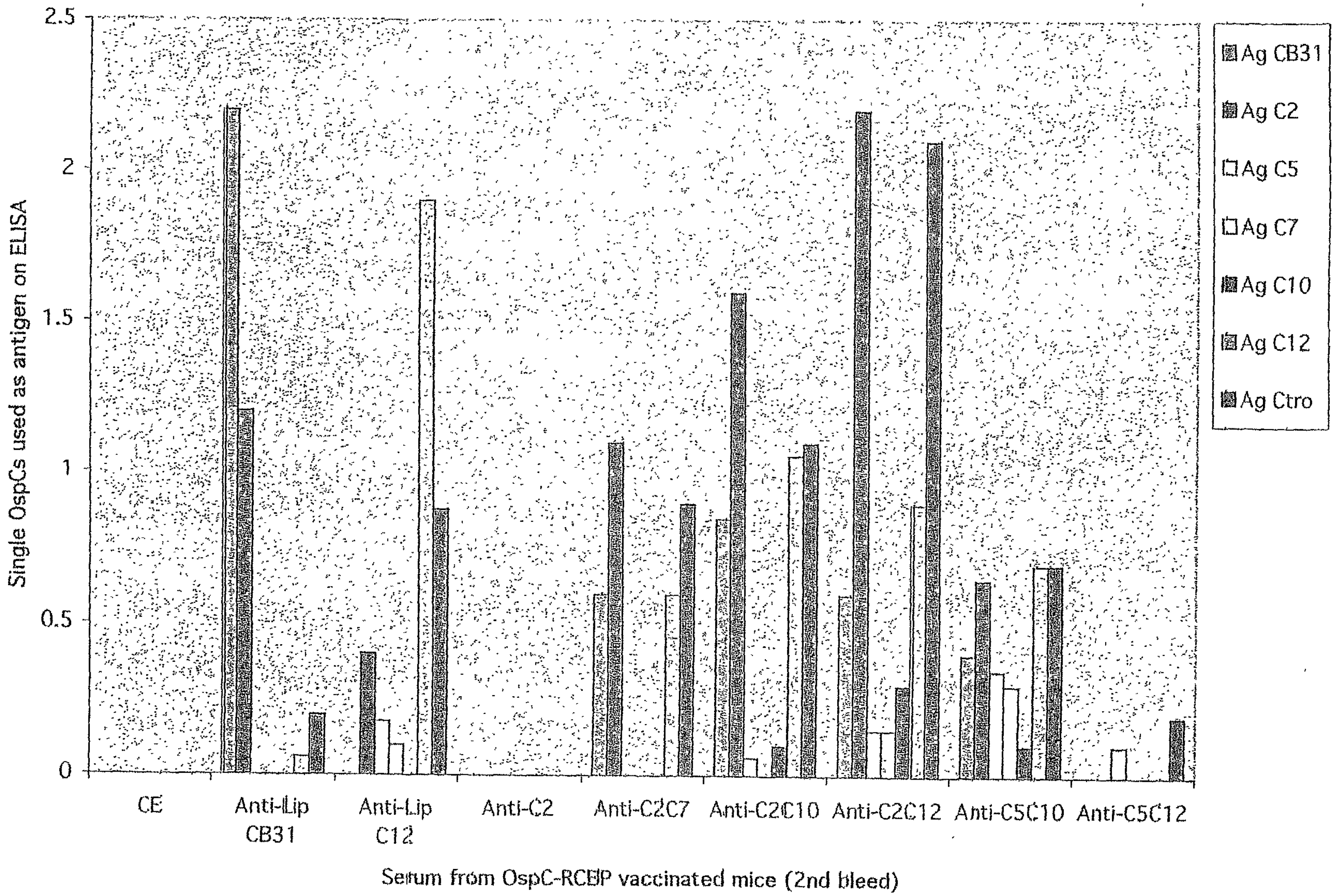


Fig. 2

09596746.061900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2
1.5
1
0.5
0
Single OspCs used as antigen on ELISA
CE
Anti-Lip CB31
Anti-Lip C12
Anti-C2
Anti-C2C7
Anti-C2C10
Anti-C2C12
Anti-C5C10
Anti-C5C12
Serum from OspC-RCBP vaccinated mice (2nd bleed)
Ag CB31
Ag C2
Ag C5
Ag C7
Ag C10
Ag C12
Ag Ctro

Fig. 3

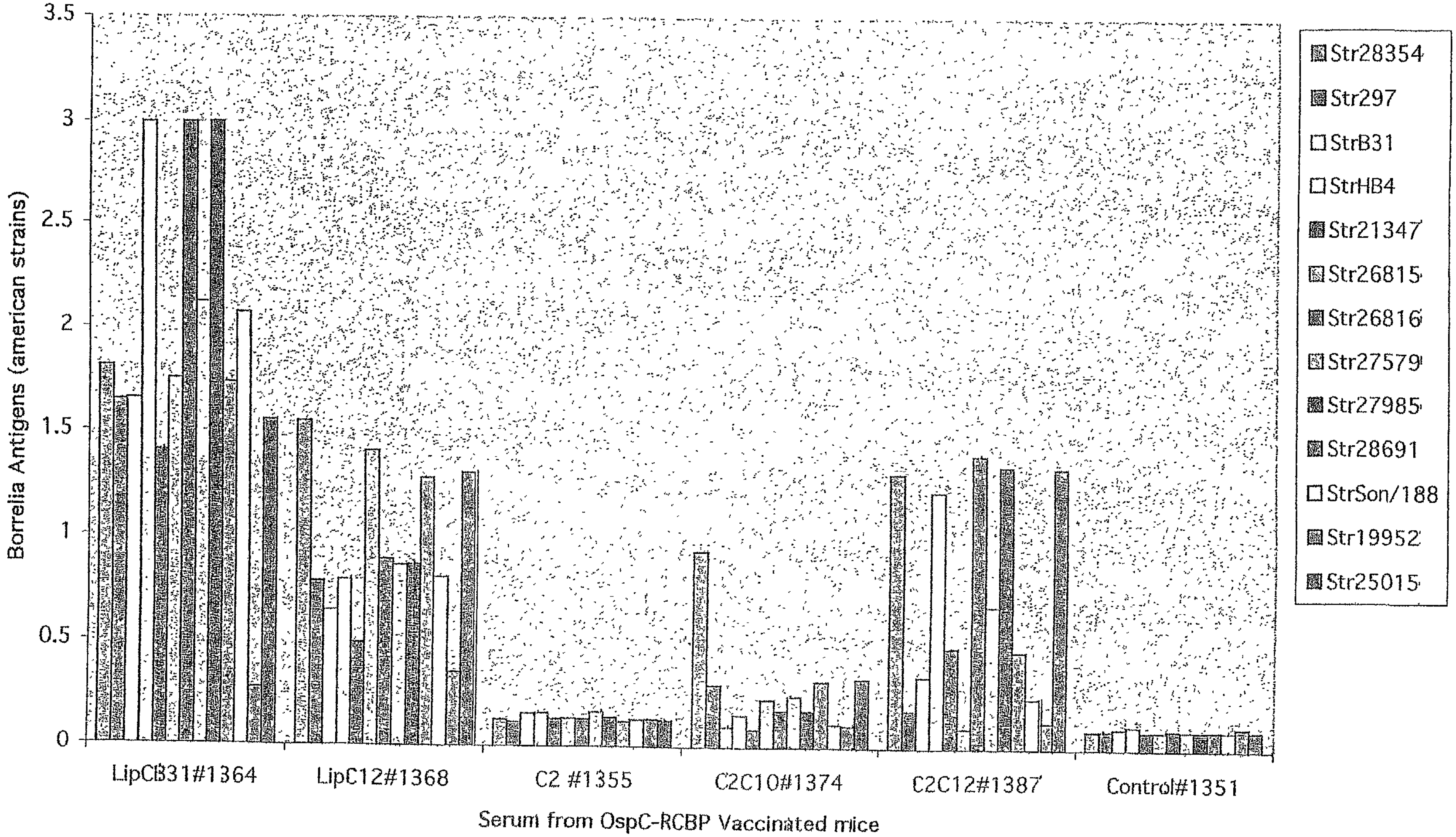
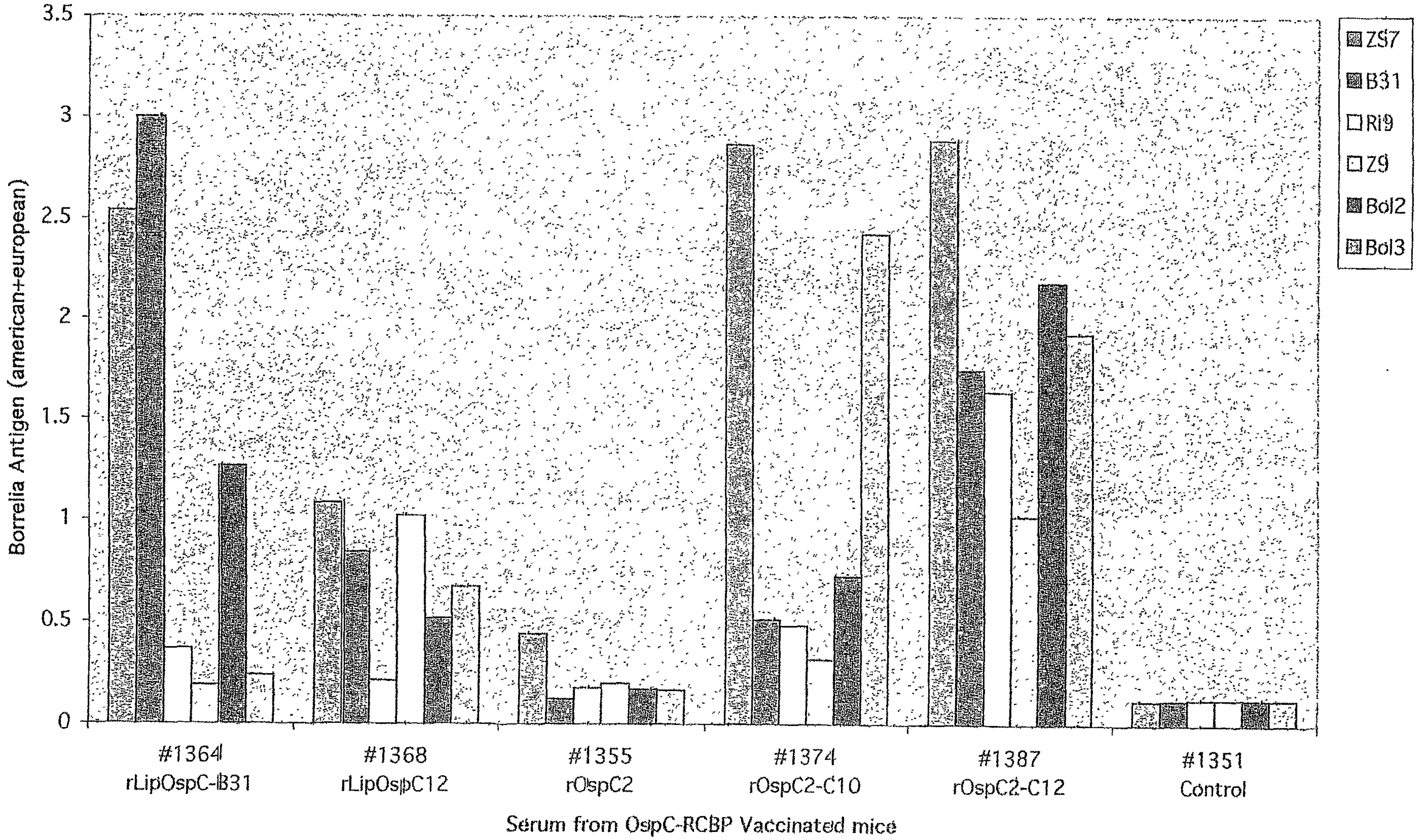


Fig. 4

09596746.061900



Borrelia Antigen (american+european)
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3
2.5
2
1.5
1
0.5
0
ZS7
B31
Ri9
Z9
Bol2
Bol3
#1364
rLipOspC-B31
#1368
rLipOspC12
#1355
rOspC2
#1374
rOspC2-C10
#1387
rOspC2-C12
#1351
Control
Serum from OspC-RCBP Vaccinated mice

Fig. 5

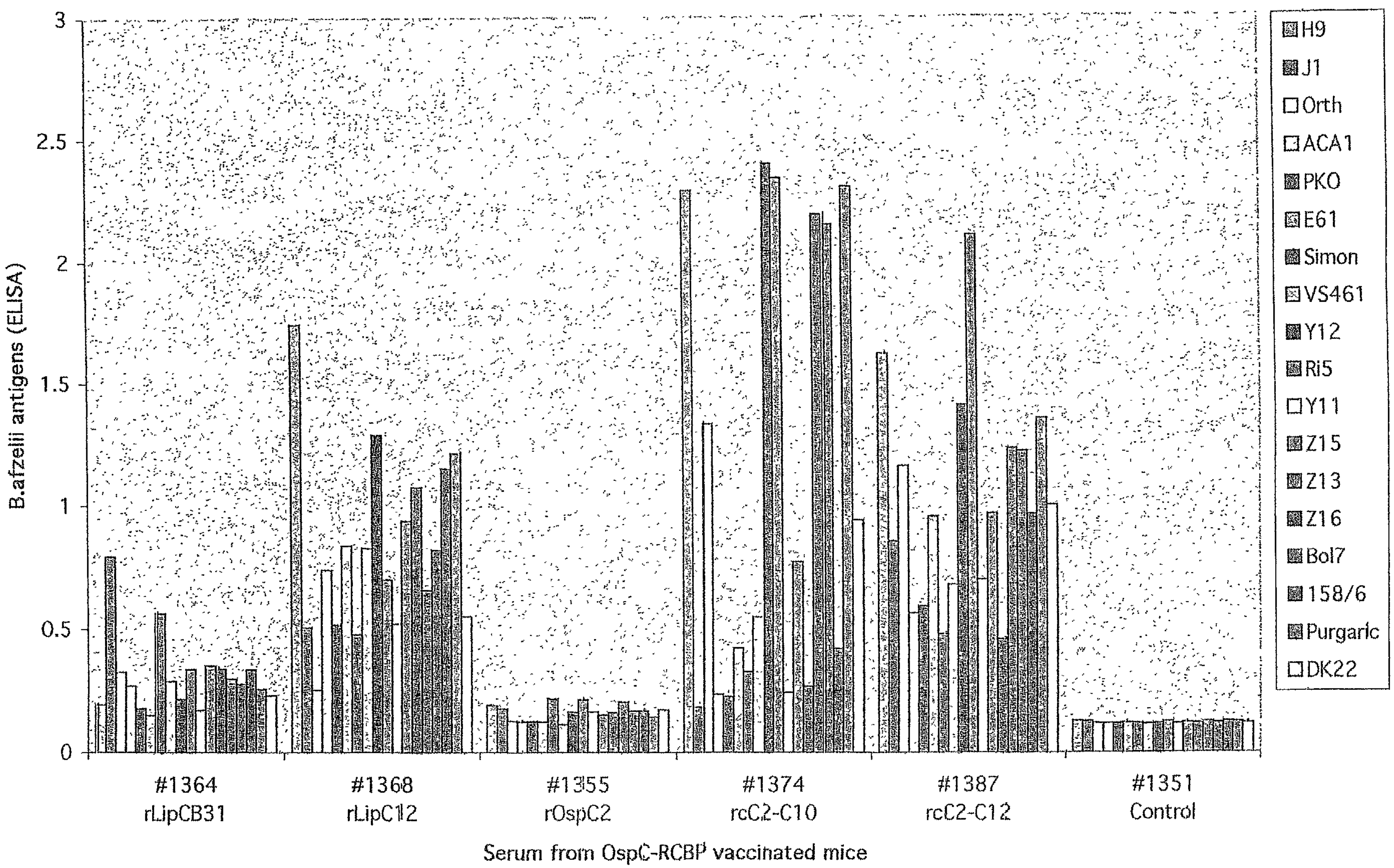
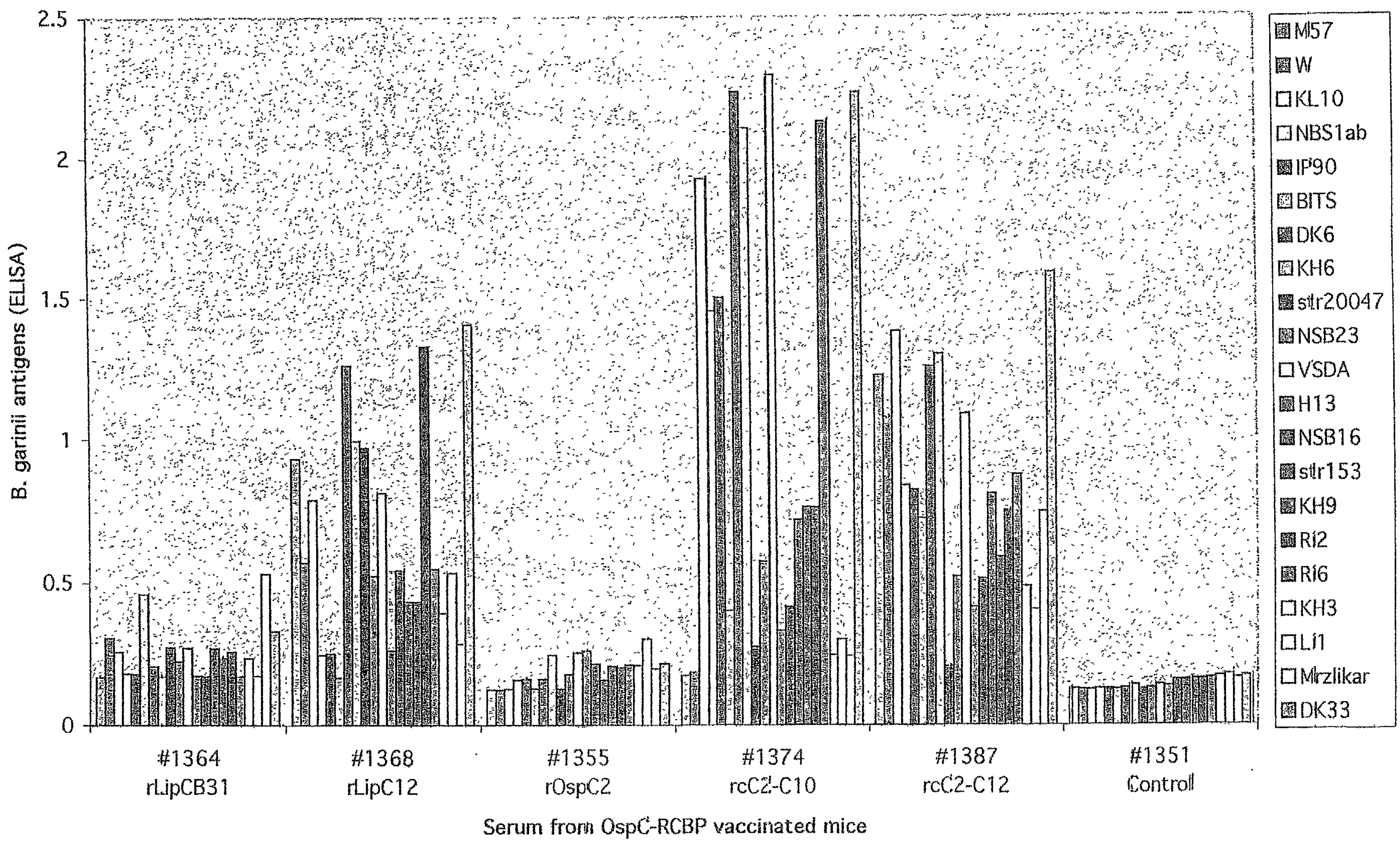


Fig. 6

09596746.061900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2
1.5
1
0.5
0
#1364
rLipCB31
#1368
rLipC12
#1355
rOspC2
#1374
rcC2-C10
#1387
rcC2-C12
#1351
Controll
Serum from OspC-RCBP vaccinated mice
MI57
W
KL10
NBS1ab
IP90
BITS
DK6
KH6
stlr20047
NSB23
VSDA
H13
NSB16
stlr153
KH9
Ri2
Ri6
KH3
Li1
Mrzlikar
DK33

Fig. 7

	Early Lyme: #P(total)				Sensitivity		Potential cross-reactivity: #P(Total Tested)				Specificity	
	EMA	EA	Ac. Dissem.	Ac. Conval.	#P(Total)	(%)	Syphilis	SLE &RA	Normals End.	Normals NonEnd.	#P(Total)	(%)
C1 (chrt1)	6(10)	ND	4(10)	8(8)	18(28)	64%	1(10)	1(10)	2(10)	0(8)	4(38)	11%
C2 (chrt2)	4(10)	ND	5(10)	8(8)	17(28)	61%	0(10)	2(10)	2(10)	0(8)	4(38)	11%
C1C10 (chrt3)	7(10)	ND	4(10)	5(8)	16(28)	57%	4(10)	1(10)	2(10)	0(8)	7(38)	18%
C1C12 (chrt4)	2(10)	ND	3(10)	5(8)	10(28)	36%	2(10)	0(10)	0(10)	ND	2(30)	7%
B31C10 (chrt5)	8(10)	ND	6(10)	5(8)	19(28)	68%	2(10)	2(10)	4(10)	0(8)	8(38)	21%
B31C12 (chrt6)	7(10)	ND	6(10)	6(8)	19(28)	68%	1(10)	1(10)	1(10)	0(8)	3(38)	8%
C2C7 (chrt7)	5(10)	6(8)	3(10)	4(7)	18(35)	51%	1(11)	0(10)	1(20)	0(8)	2(49)	4%
C2C10 (chrt8)	4(10)	7(8)	5(10)	4(7)	20(35)	57%	0(11)	0(10)	1(20)	0(8)	1(49)	2%
C2C12 (chrt9)	5(10)	7(8)	6(10)	4(7)	22(35)	63%	0(11)	1(10)	3(20)	0(8)	4(49)	8%
C5C7 (chrt10)	7(10)	ND	4(10)	5(8)	16(28)	57%	2(10)	2(10)	0(10)	ND	4(30)	13%
C5C10 (chrt11)	6(10)	ND	4(10)	5(8)	15(28)	54%	0(10)	0(10)	0(10)	ND	0(30)	0%
C5C12 (chrt12)	8(10)	ND	8(10)	6(8)	22(28)	79%	5(10)	3(10)	3(10)	0(8)	11(38)	29%

EMA = Erythema Migrans Acute
EA = Acute Disseminated
Ac. Dissem.= Acute Disseminated
Ac. Conval. = Acute Convalescent
#P = Number of positives
SLE = Systemic Lupus Erythematosus
RA = Rheumatoid Arthritis
End. = Endemic Field Workers
NonEnd. = Non Endemic

Fig. 8

SEQUENCE LISTING

<110> Dattwyler, Raymond J.
Seinost, Gerald
Dykhuizen, Danial
Luft, Benjamin J.
Maria J.C. Gomes-Solecki

<120> Groups of Borrelia burgdorferi and
Borrelia afzelii That Cause Lyme Disease in Humans

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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg    144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35                  40                  45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata    192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
    50                  55                  60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg    240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65                  70                  75                  80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt    288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
                 85                  90                  95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag    336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
            100                 105                 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag    384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
        115                 120                 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta    432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
    130                 135                 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag    480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145                 150                 155                 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt    528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
                165                 170                 175
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Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
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gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc         573
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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
        35                  40                  45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
    50                  55                  60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65                  70                  75                  80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
                85                  90                  95
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
            100                 105                 110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
        115                 120                 125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
    130                 135                 140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145                 150                 155                 160
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30
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Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
        35                  40                  45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa     192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
    50                  55                  60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg     240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65                  70                  75                  80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat     288
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                85                  90                  95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa     336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
            100                 105                 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt     384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
        115                 120                 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa     432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
    130                 135                 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt     480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145                 150                 155                 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat     528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
                165                 170                 175

gct gtt aaa gag ctt aca agt cct att gt                              557
Ala Val Lys Glu Leu Thr Ser Pro Ile
            180                 185


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Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
        35                  40                  45
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
    50                  55                  60
Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
65                  70                  75                  80
Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
                85                  90                  95
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130 135 140
His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
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Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
35 40 45

gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192
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65 70 75 80

aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
85 90 95

cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
100 105 110

aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
115 120 125

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130 135 140

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145 150 155 160

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165 170 175

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gtg 579
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35 40 45
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys
50 55 60
Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn
65 70 75 80
Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu
85 90 95
Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys
100 105 110
Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys
115 120 125
Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala
130 135 140
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 1               5                  10                  15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt      96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
            20                  25                  30

aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct     144
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
        35                  40                  45

gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa     192
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys
    50                  55                  60

gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca     240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala
65                  70                  75                  80

aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta     288
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Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu
            100                 105                 110

aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta     384
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        115                 120                 125

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Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
 1   5   10   15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
            20   25   30
Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val
        35   40   45
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala
    50   55   60
Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn
65   70   75   80
Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile
                85   90   95
Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys
            100   105   110
Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys
        115   120   125
Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala
    130   135   140
Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val
145   150   155   160
Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala
                165   170   175
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val
            180   185   190
Val

<210> 13
<211> 576
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(576)

<400> 13
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg   48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1   5   10   15

aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt   96
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
            20   25   30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc   144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
        35   40   45

gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc   192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
    50   55   60

aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag   240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65   70   75   80

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agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta     288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
                 85                  90                  95

ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag     336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
            100                 105                 110

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa     384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
        115                 120                 125

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca     432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
    130                 135                 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca     480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145                 150                 155                 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct     528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
                165                 170                 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg     576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
            180                 185                 190
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<210> 14
<211> 191
<212> PRT
<213> Borrelia burgdorferi

<400> 14
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
 1               5                  10                  15
Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
            20                  25                  30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
        35                  40                  45
Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
    50                  55                  60
Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
65                  70                  75                  80
Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
                85                  90                  95
Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
            100                 105                 110
Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
        115                 120                 125
Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
    130                 135                 140
Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
145                 150                 155                 160
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
                165                 170                 175
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Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
            180                 185                 190
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<210> 15
<211> 576
<212> DNA
<213> borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(576)

<400> 15

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atg act tta ttt tta ttt ata tct tgt aat aat tca aga aaa gat ggg     48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly
 1               5                  10                  15

aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt     96
Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
            20                  25                  30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc    144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
        35                  40                  45

gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc    192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
    50                  55                  60

aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag    240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
 65                  70                  75                  80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta    288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
                85                  90                  95

ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag    336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
            100                 105                 110

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa    384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
        115                 120                 125

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca    432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
    130                 135                 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca    480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145                 150                 155                 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct    528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
                165                 170                 175
```

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 16
<211> 191
<212> PRT
<213> borrelia burgdorferi

<400> 16
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly Asn
1 5 10 15
Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
65 70 75 80
Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
85 90 95
Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
100 105 110
Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
115 120 125
Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
130 135 140
Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
145 150 155 160
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
165 170 175
Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 17
<211> 573
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(573)

<400> 17
atg act tta ttt tta ttt ata tct tgt aat aat tca ggg aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
50 55 60

gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
65 70 75 80

gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
85 90 95

ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
100 105 110

gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
115 120 125

aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
130 135 140

gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
145 150 155 160

gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
165 170 175

gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190

<210> 18
<211> 190
<212> PRT
<213> Borrelia burgdorferi

<400> 18
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala
50 55 60
Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp
65 70 75 80
His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile
85 90 95
Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu
100 105 110

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Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys
        115                 120                 125
Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala
    130                 135                 140
Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp
145                 150                 155                 160
Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala
                165                 170                 175
Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
            180                 185                 190


<210> 19
<211> 553
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(553)

<400> 19
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg      48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1               5                  10                  15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt      96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
            20                  25                  30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct     144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
        35                  40                  45

gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act     192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
    50                  55                  60

aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa     240
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
65                  70                  75                  80

gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act     288
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
                85                  90                  95

gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa     336
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
            100                 105                 110

gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa     384
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
        115                 120                 125

tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat     432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
    130                 135                 140
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gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt 480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly
145 150 155 160

gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa 528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys
165 170 175

gcg gct aaa gag atg cta aac aag t 553
Ala Ala Lys Glu Met Leu Asn Lys
180

<210> 20
<211> 183
<212> PRT
<213> Borrelia burgdorferi

<400> 20
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu Val
65 70 75 80
Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Val
85 90 95
Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys Glu
100 105 110
Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys Leu
115 120 125
Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp Asp
130 135 140
Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly Ala
145 150 155 160
Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys Ala
165 170 175
Ala Lys Glu Met Leu Asn Lys
180

<210> 21
<211> 582
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(582)

<400> 21
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45

gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60

aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa 240
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu
65 70 75 80

gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa 288
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
85 90 95

cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag 336
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
100 105 110

gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa 384
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
115 120 125

cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag 432
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
130 135 140

aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc 480
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
145 150 155 160

gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa 528
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
165 170 175

gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct 576
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190

att gtg 582
Ile Val

<210> 22
<211> 193
<212> PRT
<213> Borrelia burgdorferi

<400> 22
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30

Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
        35   40   45
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
    50   55   60
Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala
65   70   75   80
Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu
                85   90   95
Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu
            100   105   110
Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu
        115   120   125
Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn
    130   135   140
Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala
145   150   155   160
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala
                165   170   175
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Ile
            180   185   190
Val

<210> 23
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1128)

<400> 23
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct   48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1   5   10   15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa   96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20   25   30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg   144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35   40   45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa   192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
    50   55   60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca   240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65   70   75   80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190

atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct 624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210 215 220

aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg 720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
225 230 235 240

ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa 768
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
245 250 255

aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata 816
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile
260 265 270

tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca 864
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala
275 280 285

ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa 912
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys
290 295 300

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu
305 310 315 320

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335

aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe
340 345 350

gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn
355 360 365

tca gtt aaa gag ctt aca agc taa 1128
Ser Val Lys Glu Leu Thr Ser *
370 375

<210> 24
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 24
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
180 185 190
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
195 200 205
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
210 215 220
Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu
225 230 235 240
Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn
245 250 255

Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser
260 265 270
Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile
275 280 285
Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys
290 295 300
Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly
305 310 315 320
Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
325 330 335
Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu
340 345 350
Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser
355 360 365
Val Lys Glu Leu Thr Ser
370

<210> 25
<211> 1124
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1124)

<400> 25
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175.

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190

atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210 215 220

aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
225 230 235 240

ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
245 250 255

caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
260 265 270

tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
275 280 285

gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys
290 295 300

aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
305 310 315 320

ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
325 330 335

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
340 345 350

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
355 360 365

aat tca gtt aaa gag ctt ac 1124
Asn Ser Val Lys Glu Leu
370

<210> 26
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 26
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
180 185 190
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
195 200 205
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
210 215 220
Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu
225 230 235 240
Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln
245 250 255
Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu
260 265 270
Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly
275 280 285
Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys
290 295 300
Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu
305 310 315 320

Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile
325 330 335
Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
340 345 350
Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn
355 360 365
Ser Val Lys Glu Leu
370

<210> 27
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1137)

<400> 27
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

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aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta    480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145                 150                 155                 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct    528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165                 170                 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa    576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
            180                 185                 190

aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca    624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
        195                 200                 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt    672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
    210                 215                 220

aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt    720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
225                 230                 235                 240

gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa    768
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
                245                 250                 255

aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga    816
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
            260                 265                 270

tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa    864
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
        275                 280                 285

ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag    912
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
    290                 295                 300

gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac    960
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
305                 310                 315                 320

aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc   1008
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
                325                 330                 335

att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa   1056
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
            340                 345                 350

aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg   1104
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
        355                 360                 365

ctt act aat tca gtt aaa gag ctt aca agc taa                       1137
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  *
    370                 375
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<210> 28
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 28
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1               5                  10                  15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
            20                  25                  30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35                  40                  45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
    50                  55                  60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65                  70                  75                  80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
                85                  90                  95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
            100                 105                 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
        115                 120                 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
    130                 135                 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145                 150                 155                 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165                 170                 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
            180                 185                 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
        195                 200                 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
    210                 215                 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
225                 230                 235                 240
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
                245                 250                 255
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
            260                 265                 270
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
        275                 280                 285
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
    290                 295                 300
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
305                 310                 315                 320
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
                325                 330                 335
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
            340                 345                 350
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
        355                 360                 365
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
    370                 375
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<210> 29
<211> 1133
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1133)

<400> 29
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct   48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1   5   10   15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa   96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
            20   25   30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg   144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35   40   45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa   192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
    50   55   60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca   240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65   70   75   80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta   288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
                85   90   95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag   336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
            100   105   110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat   384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
        115   120   125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta   432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
    130   135   140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta   480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145   150   155   160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct   528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165   170   175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190

aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca 624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220

aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att 720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
225 230 235 240

gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt 768
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
245 250 255

aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat 816
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
260 265 270

gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa 864
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
275 280 285

aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa 912
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
290 295 300

aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa 960
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
305 310 315 320

cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa 1008
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
325 330 335

gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt 1056
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
340 345 350

gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag 1104
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
355 360 365

atg ctt gct aat tca gtt aaa gag ctt ac 1133
Met Leu Ala Asn Ser Val Lys Glu Leu
370 375

<210> 30
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 30
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
225 230 235 240
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
245 250 255
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
260 265 270
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
275 280 285
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
290 295 300
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
305 310 315 320
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
325 330 335
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
340 345 350
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
355 360 365
Met Leu Ala Asn Ser Val Lys Glu Leu
370 375

<210> 31
<211> 1112
<212> DNA
<213> Artificial Sequence

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<220>
<223> OspC Chimera


<221> CDS
<222> (1)...(1112)

<400> 31
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct    48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1               5                  10                  15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa    96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg    144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35                  40                  45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata    192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
    50                  55                  60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg    240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65                  70                  75                  80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt    288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
                85                  90                  95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag    336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
            100                 105                 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag    384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
        115                 120                 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta    432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
    130                 135                 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag    480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145                 150                 155                 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt    528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
                165                 170                 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat    576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
            180                 185                 190

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt    624
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
        195                 200                 205
```

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aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac    672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
    210                 215                 220

gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata    720
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
225                 230                 235                 240

gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt    768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
                245                 250                 255

tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat    816
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
            260                 265                 270

gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa    864
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
        275                 280                 285

gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt    912
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
    290                 295                 300

act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt    960
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
305                 310                 315                 320

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa    1008
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
                325                 330                 335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac    1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
            340                 345                 350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt    1104
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
        355                 360                 365

aca agt cc                                                          1112
Thr Ser
    370


<210> 32
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 32
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1               5                  10                  15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
            20                  25                  30
```

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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
        35                  40                  45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
    50                  55                  60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65                  70                  75                  80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
                85                  90                  95
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
            100                 105                 110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
        115                 120                 125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
    130                 135                 140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145                 150                 155                 160
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165                 170                 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
            180                 185                 190
Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys
        195                 200                 205
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
    210                 215                 220
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp
225                 230                 235                 240
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu
                245                 250                 255
Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala
            260                 265                 270
Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu
        275                 280                 285
Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr
    290                 295                 300
Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr
305                 310                 315                 320
Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp
                325                 330                 335
Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
            340                 345                 350
Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr
        355                 360                 365
Ser
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<210> 33
<211> 1113
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1113)

<400> 33

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atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct    48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1               5                  10                  15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa    96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg    144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35                  40                  45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata    192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
    50                  55                  60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg    240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65                  70                  75                  80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt    288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
                85                  90                  95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag    336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
            100                 105                 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag    384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
        115                 120                 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta    432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
    130                 135                 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag    480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145                 150                 155                 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt    528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
                165                 170                 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat    576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
            180                 185                 190

tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt    624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
        195                 200                 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac    672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
    210                 215                 220

gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata    720
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile
225                 230                 235                 240
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gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt 768
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser
245 250 255

tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat 816
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr
260 265 270

tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca 864
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser
275 280 285

gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa 912
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu
290 295 300

ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc 960
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly
305 310 315 320

gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat 1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp
325 330 335

aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa 1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys
340 345 350

aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag 1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu
355 360 365

ctt aca agc 1113
Leu Thr Ser
370

<210> 34
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 34
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
50 55 60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65 70 75 80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
85 90 95

Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
100 105 110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
115 120 125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
130 135 140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145 150 155 160
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
180 185 190
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
195 200 205
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
210 215 220
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
225 230 235 240
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
245 250 255
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
260 265 270
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
275 280 285
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
290 295 300
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
305 310 315 320
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
325 330 335
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
340 345 350
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
355 360 365
Thr Ser
370

<210> 35
<211> 1112
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1112)

<400> 35
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

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att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg    144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35                  40                  45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata    192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
    50                  55                  60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg    240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65                  70                  75                  80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt    288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
                85                  90                  95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag    336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
            100                 105                 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag    384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
        115                 120                 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta    432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
    130                 135                 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag    480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145                 150                 155                 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt    528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
                165                 170                 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat    576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
            180                 185                 190

tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt    624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
        195                 200                 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac    672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
    210                 215                 220

gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata    720
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile
225                 230                 235                 240

gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt    768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly
                245                 250                 255

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct    816
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala
            260                 265                 270
```

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat 864
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn
275 280 285

tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa 912
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu
290 295 300

gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
305 310 315 320

aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
325 330 335

gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
340 345 350

gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
355 360 365

gag ctt ac 1112
Glu Leu
370

<210> 36
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 36
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
50 55 60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65 70 75 80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
85 90 95
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
100 105 110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
115 120 125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
130 135 140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145 150 155 160

```
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165                 170                 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
            180                 185                 190
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
        195                 200                 205
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
    210                 215                 220
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Ala Ser Ile Asp
225                 230                 235                 240
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
                245                 250                 255
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
            260                 265                 270
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
        275                 280                 285
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
    290                 295                 300
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
305                 310                 315                 320
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
                325                 330                 335
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
            340                 345                 350
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
        355                 360                 365
Leu


<210> 37
<211> 1106
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera


<221> CDS
<222> (1)...(1106)

<400> 37
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct     48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1               5                  10                  15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa     96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc    144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
        35                  40                  45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa    192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
    50                  55                  60
```

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ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg    240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65                  70                  75                  80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat    288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
                 85                  90                  95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa    336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
            100                 105                 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt    384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
        115                 120                 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa    432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
    130                 135                 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt    480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145                 150                 155                 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat    528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
                165                 170                 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga    576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
            180                 185                 190

aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg    624
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
        195                 200                 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt    672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
    210                 215                 220

gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa    720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
225                 230                 235                 240

ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag    768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu
                245                 250                 255

gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata    816
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile
            260                 265                 270

tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta    864
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu
        275                 280                 285

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat    912
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn
    290                 295                 300
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aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305 310 315 320

gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
325 330 335

ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
340 345 350

aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
355 360 365

cc 1106

<210> 38
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 38
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
180 185 190
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
225 230 235 240

Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu
245 250 255
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile
260 265 270
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu
275 280 285
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn
290 295 300
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305 310 315 320
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
325 330 335
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
340 345 350
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
355 360 365

<210> 39
<211> 1107
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1107)

<400> 39
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110

```
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt    384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
        115                 120                 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa    432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
    130                 135                 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt    480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145                 150                 155                 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat    528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
                165                 170                 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg    576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
            180                 185                 190

aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg    624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
        195                 200                 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt    672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
    210                 215                 220

gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag    720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
225                 230                 235                 240

ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat    768
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
                245                 250                 255

aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att    816
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
            260                 265                 270

tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa    864
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
        275                 280                 285

ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act    912
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
    290                 295                 300

gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act    960
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
305                 310                 315                 320

gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act    1008
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
                325                 330                 335

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg    1056
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
            340                 345                 350
```

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
355 360 365

agc 1107
Ser

<210> 40
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 40
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
35 40 45
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
50 55 60
Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
65 70 75 80
Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
85 90 95
Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
100 105 110
Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
115 120 125
Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
130 135 140
His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
145 150 155 160
Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
165 170 175
Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys
180 185 190
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
195 200 205
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
210 215 220
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu
225 230 235 240
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn
245 250 255
Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser
260 265 270
Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu
275 280 285
Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala
290 295 300
Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
305 310 315 320

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Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys
                325                 330                 335
Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser
            340                 345                 350
Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
        355                 360                 365


<210> 41
<211> 1106
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera


<221> CDS
<222> (1)...(1106)

<400> 41
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct     48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1               5                  10                  15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa     96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc    144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
        35                  40                  45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa    192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
    50                  55                  60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg    240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65                  70                  75                  80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat    288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
                85                  90                  95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa    336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
            100                 105                 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt    384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
        115                 120                 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa    432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
    130                 135                 140
```

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga 576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
180 185 190

aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220

gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa 720
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
225 230 235 240

ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta 768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
245 250 255

gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca 816
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr
260 265 270

ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa 864
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu
275 280 285

aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt 912
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe
290 295 300

act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt 960
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val
305 310 315 320

act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa 1008
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
325 330 335

gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac 1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
340 345 350

ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt 1104
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
355 360 365

ac 1106

<210> 42

<211> 367
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 42
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala
1   5   10   15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
            20   25   30
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
        35   40   45
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
    50   55   60
Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
65   70   75   80
Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
                85   90   95
Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
            100   105   110
Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
        115   120   125
Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
    130   135   140
His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
145   150   155   160
Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
                165   170   175
Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys
            180   185   190
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
        195   200   205
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    210   215   220
Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
225   230   235   240
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala
                245   250   255
Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile
            260   265   270
Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys
        275   280   285
Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr
    290   295   300
Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr
305   310   315   320
Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp
                325   330   335
Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
            340   345   350
Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
        355   360   365

<210> 43
<211> 633
<212> DNA

<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(633)

<400> 43
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atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt     48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1               5                  10                  15

ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct     96
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
            20                  25                  30

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa    144
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
        35                  40                  45

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg    192
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
    50                  55                  60

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa    240
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
65                  70                  75                  80

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca    288
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
                85                  90                  95

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta    336
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
            100                 105                 110

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag    384
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
        115                 120                 125

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat    432
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
    130                 135                 140

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta    480
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
145                 150                 155                 160

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta    528
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
                165                 170                 175

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct    576
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
            180                 185                 190

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa    624
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
        195                 200                 205
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aaa cct taa 633
Lys Pro *
210

<210> 44
<211> 209
<212> PRT
<213> Borrelia burgdorferi

<400> 44
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
1 5 10 15
Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
20 25 30
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
35 40 45
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
50 55 60
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
65 70 75 80
His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
85 90 95
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
100 105 110
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
115 120 125
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
130 135 140
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
145 150 155 160
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
165 170 175
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
180 185 190
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
195 200 205
Pro

<210> 45
<211> 580
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(580)

<400> 45
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
180 185 190

atg g 580
Met

<210> 46
<211> 192
<212> PRT
<213> Borrelia burgdorferi

<400> 46
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

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His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
65                  70                  75                  80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
                85                  90                  95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
            100                 105                 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
        115                 120                 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
    130                 135                 140
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145                 150                 155                 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
                165                 170                 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser Met
            180                 185                 190


<210> 47
<211> 639
<212> DNA
<213> Borrelia garinii

<220>
<221> CDS
<222> (1)...(639)

<400> 47
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt    48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1               5                  10                  15

ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat    96
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
            20                  25                  30

cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa   144
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
        35                  40                  45

aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag   192
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
    50                  55                  60

act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa   240
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
 65                  70                  75                  80

aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga   288
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
                85                  90                  95

tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa   336
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
            100                 105                 110

ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag   384
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
        115                 120                 125
```

```
gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat     432
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
    130                 135                 140

gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct     480
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
145                 150                 155                 160

att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa     528
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
                165                 170                 175

gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca     576
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
            180                 185                 190

cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt     624
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
        195                 200                 205

cca aaa aaa cct taa                                                 639
Pro Lys Lys Pro  *
    210


<210> 48
<211> 211
<212> PRT
<213> Borrelia garinii

<400> 48
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1               5                  10                  15
Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
            20                  25                  30
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
        35                  40                  45
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
    50                  55                  60
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
65                  70                  75                  80
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
                85                  90                  95
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
            100                 105                 110
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
        115                 120                 125
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
    130                 135                 140
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
145                 150                 155                 160
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
                165                 170                 175
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
            180                 185                 190
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
        195                 200                 205
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Lys Lys Pro
    210


<210> 49
<211> 624
<212> DNA
<213> Borrelia afzelii

<220>
<221> CDS
<222> (1)...(624)

<400> 49
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt    48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1               5                  10                  15

ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat    96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
            20                  25                  30

gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca    144
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
        35                  40                  45

gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt    192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
    50                  55                  60

tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat    240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn
 65                  70                  75                  80

gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca    288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
                 85                  90                  95

gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg    336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
            100                 105                 110

aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc    384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
        115                 120                 125

caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata    432
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile
    130                 135                 140

caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat    480
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
145                 150                 155                 160

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca    528
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
                165                 170                 175
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cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt   576
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
            180   185   190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa   624
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
        195   200   205

<210> 50
<211> 206
<212> PRT
<213> Borrelia afzelii

<400> 50
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1   5   10   15
Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu
            20   25   30
Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp
        35   40   45
Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser
    50   55   60
Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp
65   70   75   80
Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly
                85   90   95
Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn
            100   105   110
Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln
        115   120   125
Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln
    130   135   140
Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly
145   150   155   160
Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu
                165   170   175
Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys
            180   185   190
Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
        195   200   205

<210> 51
<211> 1680
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1680)

<400> 51
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct   48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1   5   10   15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190

atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 672
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
210 215 220

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
225 230 235 240

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
245 250 255

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ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg    816
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
            260                 265                 270

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg    864
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
        275                 280                 285

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct    912
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
    290                 295                 300

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca    960
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
305                 310                 315                 320

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att    1008
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
                325                 330                 335

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat    1056
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
            340                 345                 350

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta    1104
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
        355                 360                 365

act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat    1152
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
    370                 375                 380

tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc    1200
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
385                 390                 395                 400

gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg    1248
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
                405                 410                 415

aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct    1296
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
            420                 425                 430

att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat    1344
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
        435                 440                 445

cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata    1392
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
    450                 455                 460

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att    1440
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
465                 470                 475                 480
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aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat 1488
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
485 490 495

agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa 1536
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
500 505 510

aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa 1584
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
515 520 525

ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa 1632
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
530 535 540

gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca 1680
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
545 550 555 560

<210> 52
<211> 560
<212> PRT
<213> ospC Chimera

<400> 52
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
210 215 220
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
225 230 235 240

Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
245 250 255
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
260 265 270
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
275 280 285
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
290 295 300
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
305 310 315 320
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
325 330 335
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
340 345 350
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
355 360 365
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
370 375 380
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
385 390 395 400
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
405 410 415
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
420 425 430
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
435 440 445
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
450 455 460
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
465 470 475 480
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
485 490 495
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
500 505 510
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
515 520 525
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
530 535 540
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
545 550 555 560

<210> 53
<211> 1137
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1137)

<400> 53
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
225 230 235 240

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
245 250 255

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
260 265 270

tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
275 280 285

aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
290 295 300

aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
305 310 315 320

gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
325 330 335

ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
340 345 350

aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
355 360 365

cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137
Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
370 375

<210> 54
<211> 378
<212> PRT
<213> ospC Chimera

<400> 54
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
                165   170   175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
            180   185   190
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
        195   200   205
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
    210   215   220
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
225   230   235   240
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
                245   250   255
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
            260   265   270
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
        275   280   285
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
    290   295   300
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
305   310   315   320
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
                325   330   335
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
            340   345   350
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
        355   360   365
Pro Val Val Ala Glu Ser Pro Lys Lys Pro
    370   375

<210> 55
<211> 1158
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1158)

<400> 55
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct   48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1   5   10   15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa   96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20   25   30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg   144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
        35   40   45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa   192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
    50   55   60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca   240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65   70   75   80

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ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta    288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
                 85                  90                  95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag    336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
            100                 105                 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat    384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
        115                 120                 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta    432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
    130                 135                 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta    480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145                 150                 155                 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct    528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
                165                 170                 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa    576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
            180                 185                 190

aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat    624
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
        195                 200                 205

cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa    672
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
    210                 215                 220

att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct    720
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
225                 230                 235                 240

ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata    768
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
                245                 250                 255

aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg    816
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
            260                 265                 270

ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt    864
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
        275                 280                 285

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat    912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
    290                 295                 300
```

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt 960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305 310 315 320

ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa 1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335

aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt 1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
340 345 350

aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat 1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
355 360 365

tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa 1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
370 375 380

cct taa 1158
Pro *
385

<210> 56
<211> 384
<212> PRT
<213> ospC Chimera

<400> 56
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
180 185 190
Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205
Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile
210 215 220

Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu
225   230   235   240
Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys
                245   250   255
Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile
            260   265   270
Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val
        275   280   285
Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys
    290   295   300
Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly
305   310   315   320
Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
                325   330   335
His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys
            340   345   350
Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser
        355   360   365
Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
    370   375   380

<210> 57
<211> 1161
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1161)

<400> 57
atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 48
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 1   5   10   15

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20   25   30

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
        35   40   45

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
    50   55   60

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 65   70   75   80

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
                85   90   95

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
            100   105   110

```
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca     384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
        115                 120                 125

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att     432
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
    130                 135                 140

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat     480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145                 150                 155                 160

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta     528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
                165                 170                 175

act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca     576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
            180                 185                 190

aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act     624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
        195                 200                 205

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa     672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
    210                 215                 220

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag     720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225                 230                 235                 240

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa     768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
                245                 250                 255

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca     816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
            260                 265                 270

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta     864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
        275                 280                 285

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag     912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
    290                 295                 300

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag     960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305                 310                 315                 320

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta    1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
                325                 330                 335
```

```
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta    1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
            340                 345                 350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act    1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
        355                 360                 365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa    1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
    370                 375                 380

aaa cct taa                                                        1161
Lys Pro  *
385
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<210> 58
<211> 386
<212> PRT
<213> ospC Chimera

<400> 58

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Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 1               5                  10                  15
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
            20                  25                  30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
        35                  40                  45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
    50                  55                  60
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
65                  70                  75                  80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
                85                  90                  95
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
            100                 105                 110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
        115                 120                 125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
    130                 135                 140
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145                 150                 155                 160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
                165                 170                 175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
            180                 185                 190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
        195                 200                 205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
    210                 215                 220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225                 230                 235                 240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
                245                 250                 255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
            260                 265                 270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
        275                 280                 285
```

Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
290 295 300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305 310 315 320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325 330 335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380
Lys Pro
385

<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1197)

<400> 59
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

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aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat      432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
    130                 135                 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat      480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145                 150                 155                 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa      528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
                165                 170                 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca      576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
            180                 185                 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc      624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
        195                 200                 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat      672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
    210                 215                 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat      720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
225                 230                 235                 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc      768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
                245                 250                 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct      816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
            260                 265                 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag      864
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
        275                 280                 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac      912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
    290                 295                 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag      960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
305                 310                 315                 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa     1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
                325                 330                 335

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat     1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
            340                 345                 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc     1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
        355                 360                 365
```

```
gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa    1152
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
    370                 375                 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc        1197
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385                 390                 395



<210> 60
<211> 398
<212> PRT
<213> ospC Chimera

<400> 60
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1               5                  10                  15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20                  25                  30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35                  40                  45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
    50                  55                  60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65                  70                  75                  80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
                85                  90                  95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
            100                 105                 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
        115                 120                 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
    130                 135                 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145                 150                 155                 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
                165                 170                 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
            180                 185                 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
        195                 200                 205
Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly
    210                 215                 220
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
225                 230                 235                 240
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
                245                 250                 255
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
            260                 265                 270
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
        275                 280                 285
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
    290                 295                 300
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
305                 310                 315                 320
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
                325                 330                 335
```

Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
340 345 350
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
355 360 365
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
370 375 380
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390 395

<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1196)

<400> 61
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145 150 155 160

```
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa    528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
                165                 170                 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca    576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
            180                 185                 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc    624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
        195                 200                 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat    672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
    210                 215                 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat    720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
225                 230                 235                 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg    768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
                245                 250                 255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct    816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
            260                 265                 270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc    864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
        275                 280                 285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca    912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
    290                 295                 300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta    960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
305                 310                 315                 320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa    1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
                325                 330                 335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat    1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
            340                 345                 350

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag    1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
        355                 360                 365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca    1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
    370                 375                 380
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aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390 395

<210> 62
<211> 397
<212> PRT
<213> ospC Chimera

<400> 62
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
85 90 95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
100 105 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
115 120 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
130 135 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145 150 155 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
165 170 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
180 185 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
195 200 205
Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly
210 215 220
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
225 230 235 240
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
245 250 255
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
260 265 270
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu
275 280 285
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
290 295 300
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
305 310 315 320
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
325 330 335
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
340 345 350
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
355 360 365

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
    370                 375                 380
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385                 390                 395


<210> 63
<211> 1185
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1185)

<400> 63
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt    48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1               5                  10                  15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa    96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
            20                  25                  30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
        35                  40                  45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
    50                  55                  60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt   240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65                  70                  75                  80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat   288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
                85                  90                  95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca   336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
            100                 105                 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta   384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
        115                 120                 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act   432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
    130                 135                 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat   480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145                 150                 155                 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat   528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
                165                 170                 175
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aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta    576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
            180                 185                 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca    624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
        195                 200                 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct    672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
    210                 215                 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata    720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225                 230                 235                 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa    768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
                245                 250                 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt    816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
            260                 265                 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac    864
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
        275                 280                 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa    912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
    290                 295                 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa    960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
305                 310                 315                 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa    1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
                325                 330                 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa    1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
            340                 345                 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt    1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
        355                 360                 365

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag    1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
    370                 375                 380

atg ctt act aat tca gtt aaa gag ctt aca agc                        1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385                 390                 395
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<210> 64

<211> 394
<212> PRT
<213> ospC Chimera

<400> 64
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1   5   10   15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20   25   30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35   40   45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
    50   55   60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65   70   75   80
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
                85   90   95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
            100   105   110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
        115   120   125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
    130   135   140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145   150   155   160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
                165   170   175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
            180   185   190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
        195   200   205
Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
    210   215   220
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
225   230   235   240
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
                245   250   255
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
            260   265   270
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
        275   280   285
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
    290   295   300
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
305   310   315   320
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
                325   330   335
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
            340   345   350
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
        355   360   365
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
    370   375   380
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385   390

<210> 65
<211> 1184

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<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1184)

<400> 65
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt    48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1               5                  10                  15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa    96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
            20                  25                  30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
        35                  40                  45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
    50                  55                  60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt   240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65                  70                  75                  80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat   288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
                 85                  90                  95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca   336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
            100                 105                 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta   384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
        115                 120                 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act   432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
    130                 135                 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat   480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145                 150                 155                 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat   528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
                165                 170                 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta   576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
            180                 185                 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca   624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
        195                 200                 205
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agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct 672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa 768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255

att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att 816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
260 265 270

ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat 864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His
275 280 285

aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca 912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr
290 295 300

caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att 960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile
305 310 315 320

gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga 1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly
325 330 335

gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
340 345 350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
355 360 365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
370 375 380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184
Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390

<210> 66
<211> 393
<212> PRT
<213> ospC Chimera

<400> 66
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15

Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
85 90 95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
100 105 110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
115 120 125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
130 135 140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145 150 155 160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
165 170 175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
210 215 220
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
225 230 235 240
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
245 250 255
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
260 265 270
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
275 280 285
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
290 295 300
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
305 310 315 320
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
325 330 335
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
340 345 350
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
355 360 365
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
370 375 380
Met Leu Ala Asn Ser Val Lys Glu Leu
385 390

<210> 67
<211> 1184
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1184)

<400> 67

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct 672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
210 215 220

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aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata     720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225                 230                 235                 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa     768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
                245                 250                 255

gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att     816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
            260                 265                 270

ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac     864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
        275                 280                 285

aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa     912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
    290                 295                 300

aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca     960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
305                 310                 315                 320

gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat    1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
                325                 330                 335

gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct    1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
            340                 345                 350

att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa    1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
        355                 360                 365

aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca    1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
    370                 375                 380

tta aaa aat gct gtt aaa gag ctt aca agt cc                         1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
385                 390


<210> 68
<211> 393
<212> PRT
<213> ospC Chimera

<400> 68
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1               5                  10                  15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20                  25                  30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35                  40                  45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
    50                  55                  60
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Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
85 90 95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
100 105 110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
115 120 125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
130 135 140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145 150 155 160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
165 170 175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr
210 215 220
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
225 230 235 240
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
245 250 255
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
260 265 270
Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr
275 280 285
Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys
290 295 300
Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala
305 310 315 320
Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala
325 330 335
Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile
340 345 350
Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
355 360 365
Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu
370 375 380
Lys Asn Ala Val Lys Glu Leu Thr Ser
385 390

<210> 69
<211> 1209
<212> DNA
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<220>
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<222> (1)...(1209)

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atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
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1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act 672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
210 215 220

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
225 230 235 240

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
245 250 255

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gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa    816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
            260                 265                 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca    864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
        275                 280                 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta    912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
    290                 295                 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag    960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
305                 310                 315                 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag    1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
                325                 330                 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta    1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
            340                 345                 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta    1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
        355                 360                 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act    1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
    370                 375                 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa    1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
385                 390                 395                 400

aaa cct taa                                                        1209
Lys Pro  *


<210> 70
<211> 401
<212> PRT
<213> ospC Chimera

<400> 70
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1               5                  10                  15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20                  25                  30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35                  40                  45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
    50                  55                  60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65                  70                  75                  80
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Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
85 90 95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
100 105 110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
115 120 125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
130 135 140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145 150 155 160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
165 170 175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
210 215 220
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
225 230 235 240
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
245 250 255
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
260 265 270
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
275 280 285
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
290 295 300
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
305 310 315 320
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
325 330 335
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
340 345 350
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
355 360 365
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
370 375 380
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
385 390 395 400
Pro

<210> 71
<211> 1179
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1179)

<400> 71
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa     96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
            20                  25                  30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct    144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
        35                  40                  45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt    192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    50                  55                  60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt    240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65                  70                  75                  80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc    288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
                85                  90                  95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct    336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
            100                 105                 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag    384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
        115                 120                 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa    432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
    130                 135                 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat    480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145                 150                 155                 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt    528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
                165                 170                 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa    576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
            180                 185                 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct    624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
        195                 200                 205

att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat    672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
    210                 215                 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa    720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225                 230                 235                 240

aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa    768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
                245                 250                 255
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act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa 816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
260 265 270

ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca 864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
275 280 285

tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata 912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
290 295 300

agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct 960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
305 310 315 320

aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca 1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
325 330 335

gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
370 375 380

act aat tca gtt aaa gag ctt aca agc 1179
Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390

<210> 72
<211> 392
<212> PRT
<213> ospC Chimera

<400> 72
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
50 55 60
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
65 70 75 80
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
85 90 95
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
100 105 110

Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
115 120 125
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
130 135 140
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
145 150 155 160
Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
165 170 175
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
180 185 190
Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
195 200 205
Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
210 215 220
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
225 230 235 240
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
245 250 255
Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
260 265 270
Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu
275 280 285
Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser
290 295 300
Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys
305 310 315 320
Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp
325 330 335
Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu
340 345 350
Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu
355 360 365
Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr
370 375 380
Asn Ser Val Lys Glu Leu Thr Ser
385 390

<210> 73
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)

<400> 73
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

```
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt    192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
     50                  55                  60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt    240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65                  70                  75                  80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc    288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
                 85                  90                  95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct    336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
            100                 105                 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag    384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
        115                 120                 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa    432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
    130                 135                 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat    480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145                 150                 155                 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt    528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
                165                 170                 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa    576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
            180                 185                 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct    624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
        195                 200                 205

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat    672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
    210                 215                 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa    720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225                 230                 235                 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa    768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
                245                 250                 255

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa    816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
            260                 265                 270
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aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga    864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
        275                 280                 285

aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa    912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
    290                 295                 300

tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat    960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
305                 310                 315                 320

gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat    1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
                325                 330                 335

gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct    1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
            340                 345                 350

att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa    1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
        355                 360                 365

aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg    1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
    370                 375                 380

ctt gct aat tca gtt aaa gag ctt ac                                 1178
Leu Ala Asn Ser Val Lys Glu Leu
385                 390


<210> 74
<211> 391
<212> PRT
<213> ospC Chimera

<400> 74
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1               5                  10                  15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20                  25                  30
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35                  40                  45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
    50                  55                  60
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
65                  70                  75                  80
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
                85                  90                  95
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
            100                 105                 110
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
        115                 120                 125
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
    130                 135                 140
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
145                 150                 155                 160
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Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
                165                 170                 175
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
            180                 185                 190
Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
        195                 200                 205
Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
    210                 215                 220
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
225                 230                 235                 240
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr
                245                 250                 255
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
            260                 265                 270
Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr
        275                 280                 285
Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu
    290                 295                 300
Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala
305                 310                 315                 320
Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala
                325                 330                 335
Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile
            340                 345                 350
Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
        355                 360                 365
Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu
    370                 375                 380
Ala Asn Ser Val Lys Glu Leu
385                 390


<210> 75
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)

<400> 75
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt    48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1               5                  10                  15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa    96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
            20                  25                  30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
        35                  40                  45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    50                  55                  60
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ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205

att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat 672
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
210 215 220

tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag 768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
245 250 255

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag 816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
260 265 270

aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca 864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
275 280 285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta 912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
290 295 300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
305 310 315 320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
325 330 335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
340 345 350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
355 360 365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
370 375 380

aat gct gtt aaa gag ctt aca agt cc 1178
Asn Ala Val Lys Glu Leu Thr Ser
385 390

<210> 76
<211> 391
<212> PRT
<213> ospC Chimera

<400> 76
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
50 55 60
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
65 70 75 80
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
85 90 95
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
100 105 110
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
115 120 125
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
130 135 140
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
145 150 155 160
Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
165 170 175
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
180 185 190
Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
195 200 205

Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser
210 215 220
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
225 230 235 240
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
245 250 255
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
260 265 270
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
275 280 285
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
290 295 300
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
305 310 315 320
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
325 330 335
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
340 345 350
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
355 360 365
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
370 375 380
Ala Val Lys Glu Leu Thr Ser
385 390

<210> 77
<211> 1230
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1230)

<400> 77
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

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acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata    336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
            100                 105                 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta    384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
        115                 120                 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat    432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
    130                 135                 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat    480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145                 150                 155                 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa    528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
                165                 170                 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca    576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
            180                 185                 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc    624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
        195                 200                 205

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca    672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
    210                 215                 220

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct    720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
225                 230                 235                 240

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta    768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
                245                 250                 255

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt    816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
            260                 265                 270

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac    864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
        275                 280                 285

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca    912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
    290                 295                 300

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag    960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
305                 310                 315                 320
```

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
325 330 335

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
340 345 350

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
355 360 365

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
370 375 380

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
385 390 395 400

gtt gtg gca gaa agt cca aaa aaa cct taa 1230
Val Val Ala Glu Ser Pro Lys Lys Pro *
405

<210> 78
<211> 408
<212> PRT
<213> ospC Chimera

<400> 78
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
85 90 95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
100 105 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
115 120 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
130 135 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145 150 155 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
165 170 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
180 185 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
195 200 205
Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser Gly
210 215 220

Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn
225 230 235 240
Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu
245 250 255
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser
260 265 270
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu
275 280 285
Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys
290 295 300
Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys
305 310 315 320
Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu
325 330 335
Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn
340 345 350
Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala
355 360 365
Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala
370 375 380
Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val
385 390 395 400
Val Ala Glu Ser Pro Lys Lys Pro
405

<210> 79
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1209)

<400> 79
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
210 215 220

ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
225 230 235 240

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
245 250 255

gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
260 265 270

gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
275 280 285

gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
290 295 300

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
305 310 315 320

gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008

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Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
                325                     330                     335

act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt     1056
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
            340                 345                     350

act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa     1104
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
        355                     360                 365

act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac     1152
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
    370                     375                 380

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt     1200
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
385                 390                     395                 400

aca agc taa                                                         1209
Thr Ser  *



<210> 80
<211> 401
<212> PRT
<213> ospC Chimera

<400> 80
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1               5                  10                  15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
            20                  25                  30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
        35                  40                  45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
    50                  55                  60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65                  70                  75                  80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
                85                  90                  95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
            100                 105                 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
        115                 120                 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
    130                 135                 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145                 150                 155                 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
                165                 170                 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
            180                 185                 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
        195                 200                 205
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
    210                 215                 220
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Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
225 230 235 240
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
245 250 255
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
260 265 270
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
275 280 285
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
290 295 300
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
305 310 315 320
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
325 330 335
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
340 345 350
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
355 360 365
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
370 375 380
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
385 390 395 400
Ser

<210> 81
<211> 1205
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1205)

<400> 81
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

```
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata    336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
            100                 105                 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta    384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
        115                 120                 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat    432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
    130                 135                 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat    480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145                 150                 155                 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa    528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
                165                 170                 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca    576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
            180                 185                 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc    624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
        195                 200                 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca    672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
    210                 215                 220

gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa    720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
225                 230                 235                 240

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca    768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
                245                 250                 255

gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat    816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
            260                 265                 270

gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt    864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
        275                 280                 285

tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat    912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
    290                 295                 300

aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca    960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
305                 310                 315                 320
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gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat 1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
325 330 335

ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat 1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
340 345 350

gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
355 360 365

aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
370 375 380

aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
385 390 395 400

ctt ac 1205
Leu

<210> 82
<211> 400
<212> PRT
<213> ospC Chimera

<400> 82
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
85 90 95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
100 105 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
115 120 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
130 135 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145 150 155 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
165 170 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
180 185 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Raymond J. Dattwyler, Gerald Seinost, Daniel Dykhuizen, Benjamin J. Luft and Maria J. C. Gomes-Solecki

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA AFZELII THAT CAUSE LYME DISEASE IN HUMANS

TRANSMITTAL OF SEQUENCE LISTING IN COMPUTER READABLE FORM IN COMPLIANCE WITH 37 C.F.R. §§1.821(e) AND (f)

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith is a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicant's Attorney hereby states that the content of the "Sequence Listing" in paper form and of the computer readable form of the "Sequence Listing" are the same.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

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Date: June 19, 2000